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Maximum Match 100%
Listing first 45 summaries
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1: gb ba:*
2: gb htg:*
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5: gb ov:*
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7: gb ph:*
9: gb pr:*
10: gb ro:*
11: gb sts:*
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11: gb sts:*
12: em hum:*
13: gb un:*
14: gb vi:*
16: em fun:*
17: em hum:*
18: em on:*
19: em pat:*
6: em fu:*
19: em htg hum:*
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10160.111 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AUTHORS KO		ORGANISM Ho	SOURCE Ho	KEYWORDS JP	VERSION BD	ACCESSION BD	1e	DEFINITION IS	LOCUS BD	BD205033	KESCLT L
Losses 1 to 5199/ Korenberg, J.R. and Chen, X.N. Isolated SH3 gene relating to myeloproliferative disorders and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	JP 2002511267-A/1.	BD205033.1 GI:33014803	BD205033	leukemia and utilization thereof.	Isolated SH3 gene relating to myeloproliferative disorders and	BD205033 5199 bp DNA linear PAT 17-JUL-2003		

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Patent: JP 2002511267-A 1 16-APR-2002;
CEDARS SINAI HEALTH SYSTEM ET AL
OS Homo sapiens (human)
PN JP 2002511267-A/1
PD 16-APR-2002
PF 16-APR-1999 JP 2009543610
PR 16-APR-1998 US 60/082007
PI JULIE R KORENBERG, XIAO NING CHEN
PC C12N15/99, A01K67/027, C07K14/47, C07K1
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G01N33/68//A61K48/00,C12N15/00,C12N5/00
Isolated SH3 gene relating to myeloproliferative disorders
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16-APR-1999 JP 2000543610

16-APR-1998 US 60/082007

JULIE R KOREMBERG, XIAO NING CHEN

C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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Key Location/Qualifiers

source 1. | .5199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHT KOATA
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/70
PN JP 2002017375-A/70
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAWATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
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1 (bases 1 to 877)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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mer for synthesizing full-length cDNA and use thereof FH 1
Location/Qualifiers
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live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer for synthesizing full-length cDNA and use thereof
patent: JP 2002017375-A 1639 22-JAN-2002;

Patent: JP 2002017375-A 1639 22-JAN-2002;

Homo sapiens (human)
JP 2002017375-A/1639
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PF 1SHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII
JURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
112N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 877)
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                      CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC
                                                                                                           AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC
                                                                                                                            AAGTAACAGAACCATGGCTCAGTTTTCCAACACCTTTTTGGTGGCAGCCTGGATATCTGGGC
                                                                                                                                                                 TTTGTCCCTGGGGCGCAGCGCGGACCCGGCCGGAGATGAGGCGTCGATTAGCAAGGTAA
                                                                                                                                                                                                                                                                               TTTGTCCCTGGGGCGGCAGCGCGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism='Homo
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Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 82 Row: 1 Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens, Similar to intersectin 1 (SH3 domain protein), IMAGE: 5784342, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: National Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: ht
Contact: MGC help desk
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/product="Similar to intersectin
/protein_id="AAH39036.1"
/db_xref="GI:27371135"
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/clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5784342"
                                                                                      /codon_start=1
                                                                                                                                                 /note="Vector:
                                                                                                                                                                                   /lab host="DH10B"
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                            Primer for synthesizing five tent: JP 2002017375-A 3 HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017375-A/3071 PD 22-JAN-2002 PF 07-JUL-2000 JP 200021 PF 1 TOSHIO OTA, TETSUO NIC
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                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1676)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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JP 2002017375-A/3071.
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Primer for synthesizing
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22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                      Homo sapiens (human) JP 2002017375-A/3071
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                                                                                                                                           full-length cDNA and 3071 22-JAN-2002;
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full-length
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nd use thereof.
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Best Local
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Homo sapiens cDNA FLJ90809 fis, c
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PI YURI KAWAI,AI WAKAMATSU,TOM
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC
                                                                    AK075290
AK075290.1 GI:22761283
oligo capping; fis (full insert sequence)
                                               Homo sapiens
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                                    Eukaryota;
                                                         Homo sapiens (human)
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Isogai,T.,
                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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mer for synthesizing full-length cDNA and use thereof FH I
Location/Qualifiers
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YURI KAWAI,AI WAKAMATSU,TOMOYASU
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                       ; Metazoa;
Eutheria;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Ota,T.,
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Nishikawa,T.,
                       Chordata;
Primates;
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Pred. No. 1.5e-116;
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                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                            clone Y79AA
g form mRNA.
Hayashi, K.,
                                                                                                                                   mRNA
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                                     Euteleostomi;
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TITLE
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JOURNAL
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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Tokyo Carter)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.
Ninomiya, K.
NEDO human cDNA sequencing project
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Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Location/Qualifiers
                                                                 500
                                  556
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/clone_lib="Y79AA1"
/note="cloning vector: pME18SFL3"
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/cell_line="Y79"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                  GGGATGGTGTGCGGGCTGCGGCTCCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
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 GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC
                                                                                                                                     CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC
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                                    TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT
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97.2%;

0,

Score 486; DB 6; L Pred. No. 1.6e-116; 0; Mismatches 0;

Length 2131; Indels

0;

Gaps

333 194 273 134 213

434

513 374 453 314 393 254

494 573

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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Sigiyama,T., Wakamatsu,A., Nagai,K. Primers for synthesising full-length cDNA and Patent: EP 1074617-A 15558 07-FEB-2001; Research Association for Biotechnology (JP)
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                      /codon_start=1
//protein_id="CAE92347.1"
//protein_id="CAE92347.1"
//protein_id="CAE92347.1"
//db_xref="rd1:40035490"
//translation="MAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQA
//translation="MAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQA
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RNFFFQSGLPQFVLAQJWALADMUNDGRMDQVEFSIAMHJFKSSSFSGQFGSQLWTK
LQKAQSFDVASVPPVAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLP
QAQLASIWNLSDIDQDGKLTAEFFILAMHLIDVAMSQGPLPFVLFPEYIFPSFRRVRS
GSGISVISSTSVDQBLPEEPYLEDEQQQLEKKLPVTFEDKKRENEFGRULELEKRRQA
LLEQQRKEQERLAQLERAEQERKERERQBEGEKKRQLELEKQLEKGRETEBRK
EIERREAAKRELERQRQLEWERNRRQELLNGRNKEGEDIVTLKKKKTLEFELEALND
KKHQLEGKLQDIRGLTTGRGEISSTNKSRELKIAEITHLQQQLGESQOMLGRLIFBK
QILNDQLKQVQQNSLHRDSLVTLKRALEAKELARQHLRDQLDEVEKETRSKLQEIDIF
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NNQLKELREIHNKQQLQKQKSMEAERLKQ"
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/db_xref="taxon:9606"
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Primer for
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PI TETSUJI OTSUKI,HISASHI KOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chdrdata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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JP 2002017375-A/2599.
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                                                                           AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC
                           CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC
                                                                                                                                                             GGGATGGTGTGCGGGCTGCGGTCCCTCCCAGCGGCGCGTGAGCGGCACTGA
             CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC
                                                                                                             TTTGTCCCTGGGGCGCAGCGCGGACCCCGGAGATGAGGCGTCGATTAGCAAGGTAA
                                                                                                                                  TTTGTCCCTGGGGCGGCGGGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194
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ner for synthesizing full-length cDNA and use thereof FH 1
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Homo sapiens (human)
JP 2002017375-A/2599
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /organism="Homb sapiens"
/mol_type="genbmic DNA"
/db_xref="taxoh:9606"
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(205)..(2130).
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100.0%;
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1 (bases 1 to 2131)

10 to 7... Isogai, T. Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent; JP 2002191363-A 13413 09-JUL-2002; HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)
PN JP 2002191363-A/13413
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PF XBITO, OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI
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                                                                                                                                                                               GGGATGGTGTGCGGGCTCCTGCGTCCCTCCCAGCGGCGCGTGAGCGGCACTGA
                                                                                                                                                                                                                                                   AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC
                                                                                                                                                  GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCTCCCAGCGGCGCGTGAGCGGCACTGA
                                               TTTGTCCCTGGGGCGGCAGCGGGACCCGGCCGGAGATGAGGCGTCGATTAGCAAGGTAA
                                                                                                TITGTCCCTGGGGGGGGAGGGGGACCCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for synthesizing full-length Location/Qualifiers (347). (2131).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                        486;
    Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Sylvan institute (supported by Japan Key Technology Center etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Mishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Kanehori,K.
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Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                               University of Tokyo.
                                                                                                                                                                                                                                                                                                                                 and Department of Virology, Institute of Medical Science,
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                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                   /note="cloning
                                                                                                                                                     /tissue_type="placenta"
/clone_lib="PLACE1"
                                                                                                                                                                                             /clone="PLACE1010942"
                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                        97.2%;
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                                                      Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                   Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa, Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                        Isogai, T. and Otsuki, T.
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                                                                                                                                                                                                                                                                                          (bases 1 to 2131)
    organism="Homo sapiens"/
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 03-SEP-2002
highly similar
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Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 2199)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                BC058925.1
                                                                                                                                                                                                                                                                                                             IMAGE: 4443129),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                TGCACT 497
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/tlssue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
/dev_stage="embryo, 10 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="cloning vector: pME18SFL3"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                GI:37589134
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Pred. No. 1.6e-116;
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(SH3)
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                                                                                                                                                                                                                                                                                                                                           linear
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyere, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Series: IRAK Plate: 119 Row: b Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies,
CDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .nfo@bcgsc.bc.ca
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/translation="MAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQA RNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFSIAMKLIKLKQTYQLPSALPPWA KQQPVAISSAPARGMGGIASMPPLTAVAPVPMS IPVVGMSTLVSSVPTAAVVPLAW KQQPVIQPLPAFAHFPAGTLPKSSSFSRSGFGGQLNTKLQKAQSFDVASVPDVAEWAVP QSSRLKYRQLENSHDKIMSGHITGPGARTILMQSSLPQAQLASIWNLSDIDQDGKLTA EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPV
                                                                                                                                                                                                                   /db_xref="LocusID:6453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonyms: ITSN, /db_xref="LocusID:6453" /db_xref="MIM:602442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Liver, adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene=":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ITSN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:4443129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.lln1.gov
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FEATURES

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REMARK COMMENT

REFERENCE AUTHORS TITLE

PUBMED

JOURNAL

JOURNAL MEDLINE

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                   RESULT 13
BD205035
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Leukemia and utiliz
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JP 2002511267-A/3.
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Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 5195)

Korenberg, J. R. and Chen, X. N.
Isolated SH3 gene relating to myeloproliferative discleukemia and utilization thereof Patent: JP 2002511267-A 3 16-APR-2002;
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JP 2002511267-A/3
16-APR-2002
16-APR-1999 JP 2000543610
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JULIE R KORENBERG, XIAO NING C
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Isolated SH3 gene relating to myeloproliferative
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1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Castelldefels km. 2,7, Barcelona 08907, Spain
Location/Qualifiers
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VTKKDGDWMTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVVIASYTAT
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RNRROELLNORNKEOBDI VOLKAKKYLEFELBALNDKHOLEGOLODI RCRLTTORO
EIESTMEKSRELRIAHT IHLOQOLOESOOMLGRLI PEKOI LNDOLKOVOONSLHRDSLV
TLKRALEAKELAROHLRDOLDEVEKETRSKLOEI DI FNNQLKELREI HNKOOLOKOKS
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GAPPVIQPLPAFAH
PAATLEKSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVP
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KREES VKKKDGEBKÍKOEAQDKLGRLFHOHOBEAK PA VOA PMSTA EKGELTI GAGENV
KVVYYRALY IP ESRÍHDE IT I OPGDI I MVKGEMVDESOTGE POWLGGELKKGKTOFPE
NYAEKI PENEVPAPÍKEVTOSTSAPAPKLALRETPAP LAVTSSEPSTTPNNWADFSST
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EEFILAMHLIDVAMSGQÞLÞÞVLÞÞEYIÞÞSYIRSGSGISVISSTSVDQRLÞEEÞV
LEDEQQQLEKKLÞVTÞEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQE
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            Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5458)

Korenberg, J. R. and Chen, X. N.

Isolated SH3 gene relating to myeloproliferative disorders and leukemia and utilization thereof
Patent: JP 2002511267-A 2 16-APR-2002;
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CATAACTGTAGAGGAAAGAGCGAAGGCATGATCAGCAGTTCCATAGTTTAAAGCCCAATATC
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Key Location
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JULIE R KORENBERG,XIAO NING CHEN
C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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JP 2002511267-A/2
16-APR-2002
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16-APR-1998 US 60/08200
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554 TGCACT 559	495 TGCACT 500	494 GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC 553	435 GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC 494	434 TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGAAGAATGGATCAAGT 493	375 TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAATGAAT	374 TGGATTCATTACTGGTGATCAAGCTAGAAACTTTTTTTTT	315 TGGATTCATTACTGGTGATCAAGCTAGAAACTTTTTTTTT	314 CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC 373	255 CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC 314	254 AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC 313	195 AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC 254	194 TTTGTCCCTGGGGCGCAGCGCGGACCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 253	135 TTTGTCCCTGGGGCGGCAGCCGGGACCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194	134 GGGATGGTGTGCGGGCTGCGGCTCCCTGCGAGCGGCGCGTGAGCGGCACTGA 193	75 GGGATGGTGTGCGGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGAATGA 134

Search completed: July 1, 2004, 12:16:42 Job time : 2138 secs

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(c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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486 486 484.4 474	:
	% Query Match
	% Query Match Length DB ID
13 12 13	
BQ941336 BQ050397 BQ941411 BG118422	ID
	Description

ALIGNMENTS

REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT 1 BQ941336 COMMENT DEFINITION JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 896)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999) Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLCM2594 row: k column: 01 BQ941336.1 EST. BQ941336 896
AGENCOURT_8741326 NIH_MGC_18
5', mRNA sequence.
BQ941336 Plate: LLCM2594 row: k column: High quality sequence stop: 763. Homo sapiens Contact: Robert Strausberg, Ph.D. Homo sapiens (human) GI:22356814 bp mRNA Homo sapiens mRNA linear EST 21-AUG-2002 CDNA clone IMAGE:6420600 bе

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                                                                                        5', mRNA sequence.
BQ050397
BQ050397.1 GI:19809737
                                                      Homo sapiens
                                                                 Homo sapiens (human)
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/tlosue_type="large_cell_carcinoma"
/lab_host="DH1DB (phage-resistant)"
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/clone_lib="NHH MGC_18"
/clone_Corgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORIXhol sites using the following 5; adaptor:
GGCACGAG(G): Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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BGENCOURT_8744157 Lupski_sciatic_nerve Homo sapiens
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Query Match
Best Local Similarity
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Mational Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.mih.gov
Tissue Procurement: ATCC
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Plate: LLAM12869 row: 1 column: 07
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                                                                                                                       GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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National Institutes of Health, M
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Plate: LLAM13629 row:
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                                                                                                                                      AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC
                                                                                                                                                                             TTTGTCCCTGGGGCGGCAGCGCGGACCCCGGAGATGAGGCGTCGATTAGCAAGGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sil
NotI; Site 2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
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/lab_host="DH10B"
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/mol_type="mRNA"
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/dev_stage="adult, 70 yr"
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Pred. No. 2e-115;
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Local Similarity
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National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: LLAM10216 row: p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG118422.1 GI:12611928
                                                                                                                                         GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
                                                                                                                                                                                                                                           GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC 494
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TTTGTCCCTGGGGCGGCAGCGCGGACCCCGGAGATGAGGCGTCGATTAGCAAGGTAA
                                         TTTGTCCCTGGGGCGGCAGCGGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194
                                                                                             GGGATGGTGTGCGGGCTCCTGCGTCCCTCCCAGCGGCGCGTGAGCGGCACTGA
                                                                                                                                                                                            (bases 1 to 750)
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                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db xref="taxon:9606"
/dlone="MAGE:4443129"
/clone="MAGE:4443129"
/tissue_type="adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 90"
/clone_lib="NHH MGC 90"
/clone="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
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                                                                                                                                                                                                                                                                                                                 94.8%;
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                                                                                                                                                                                                                                                                                            Score 474; DB 12;
Pred. No. 9.4e-113;
0; Mismatches 0;
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s cDNA clone IMAGE:4443129
                                                                                                                                                                                                                                                                                                                                        Length 750;
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TITLE
JOURNAL
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                                                                                                                  Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                      Schein, Duane Smarre, Michael Thorne, Miranada Tsai, Michael Thorne, Scott Zuyderduyn,
                                                                                                                                                                                                                                                                              info@bogsc.bc.ca
info@bogsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Dorraine Spence, Jeff Stott,
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, clone IMAGE:4899011, BC020269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 2126)
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                             Location/Qualifiers
1. .2126
                                                                                                                                                                                                                                                                   Natasja van den Bosch,
Marco Marra.
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                  AGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTCTGCACT
                                                                                   GATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTTCCAT
                                                                                                                                                                                                                                                                                      CATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGA
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                                                                                                                            TGGTGATCAAGCTAGAAACTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Pancreas,
/clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4899011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 474; DB Pred. No. 1.200; Mismatches
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SOURCE
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                                                                 REFERENCE
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                                                                                                                                                  KEYWORDS
                                                                                                                                                                     VERSION
                                                                                                                                                                                   ACCESSION
                    TITLE
                                                     AUTHORS
                                                                                                                                                                                   EX470886
DKFZp686E17123 r1 686 (synonym: h
nKFZp686E17123 5', mRNA sequence.
Bahr, A., Lauber, J., Mewes, H.W., Weil, Fobo, G., Han, M. and Wiemann, S. EST (Bahr, A., Lauber, J., Mewes, H.W., Unpublished (2003)
                                                                 Mammalia; Eutheria;
1 (bases 1 to 643)
                                                                                                                   Homo sapiens
                                                                                                                                                                 BX470886.1
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                 GI:31665209
                                                Mewes, H.W., Weil, B.,
                                                                                  Primates;
                                                                               Catarrhini; Hominidae;
                                                                                                                                                                                                                hlcc3) Homo sapiens
                 Weil, B.,
                                                Amid, C.,
                                                 Osanger, A.
                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                   EST 04-SEP-2003
                                                                                                                                                                                                                  clone
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This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Can Research Center (DKFZ); Beail s. wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequenc. consortium of the German Genome Project.

sequencing

Cancer

Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg,

Germany

No s1 sequence available.

This clone (DKFZp686E17123) is available at the RZPD in Please contact the RZPD Ressourcenzentrum, Heubnerweg 6 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

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REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
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BG829540
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National Institutes of Health, M
Unpublished (1999)
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 811)
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602763842F1 NIH_MGC_42 Homo sapiens
                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Preparation: Ling Hong/Rubin Laborator CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informat
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/db_xref="taxon:9606"
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/note="Vector: pTriplEx2;
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/lab_host="DH10B"
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Pred. No. 4.1e-109;
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http://image.llnl.gov
plate: LLCM1790 row: c colu
High quality sequence stop: (
                                                                                       DKFZp686K1884_r1 686 (synonym: DKFZp686K1884_5', mRNA sequenc AL711737
                          Homo sapiens
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Mammalia;
             Eukaryota;
                                                                         AL711737.1
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
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/db_xref="taxon:9606"
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Eutheria;
             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                          GI:19695092
                                            (human)
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Primates;
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Pred. No. 4.9e-109;
0; Mismatches 2;
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sequence
                   troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please contact the RZPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp686K18\beta4) is available at the RZPD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No s1 sequence available
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                                                                                                                                                             AACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTCTGCACT 500
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/db_xref="taxoh:9606"
/clone="DKFZp696K1884"
/dev_stage="adhlt"
/lab_bost="DH108"
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Location/Qualifiers
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
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Pred. No. 1.4e-107;
                605 bp mRNA linear EST 28-FEB:
7.ab1 Chimpanzee brain library Koos Pan
12B22043_rev_1_A05_r_037.ab1 5', mRNA
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1 (bases 1 to 605)
Hellmann, I., Zollner, S., Enard, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: paabo@eva.mpg.de
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deutscher Platz 6, 04103 1
Tel: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res.
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Mammalia; Eutheria; Primates;
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     AGCTACAAGGATATCAGCTACCCTCTGCACT
                                                           ATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGA
                                                                                                        TTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGA
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                                       ATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGA
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/lab_host="Epicurian Coli (TM) XL-10-Gold"
/clone lib="Chimpanzee brain library Koos"
/clonetor: pUChi; Site_1: Sfil-A; Site_2: Sfil-B; The
library was prepared using the SMART cDNA library
construction Kit (Clontech), doing only primer extension,
but not PCR amplification of the cDNA. The only deviation
from the published protocoll was that we cloned the cDNA
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Pred. No. 3.2e-103;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAK Plate: 14 Row: c Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genemics Office, Mational Cancer Gene Collection (MGC), Cancer Genemics Office, National Cancer Genemics Office, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC013578.1 GI:15488896
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IMAGE:3878242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute, 31 Center Drive, Room 11A03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTACAAGGATATCAGCTACCCTCTGCACT
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  TAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTG
                                      TAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTG
                                                                                                                                           GTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCA
                                                                                                                                                                                               TGTCCCTGGGGCGGCAGCGGGACCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAAAA
                                                                                                                                                                                                                                              TGTCCCTGGGGCGGCAGCGGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAAAA 196
                                                                                                                                                                                                                                                                                                  GATGGTGTGCGGGCTGCGTCCTGCGTCCCCAGCGGCGCGTGAGCGGCACTGATT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3878242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Lung, large cell carcinoma"
/clone_lib="NIH_MGC_68"
/lab_host="DH10B"
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Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB269754 734 bp mRNA linear 1008661 Human Fat Cell 5'-Stretch Plus cDNA Library cDNA 5', mRNA sequence.
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Seq primer: GTTGGTACCCGGGAATTC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dgong@medicine.umaryland.edu
                                                                                                                                                                                                                                                                                                                                                                          Similarity
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/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
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Pred. No. 7.8e-97;
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 62
                                                                                                             44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: libin@helix.nih.gov
DNA Sequencing and analyses by Mational
Intramural Sequencing Center (NISC).
Plate: 02 row: g column: 02
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI750406 and AI750406 mRNA linear EST 20-JUN-cn02902.x2 Normal Human Trabecular Bone Cells Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A. SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301-402-4877
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10/10C101, 9000 Rockville Pike,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medical Genetics Branch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)
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                       GTCCCTCCCAGCGGCGCGTGA¢CGGCACTGATTTGTCCCTGGGGCGGCAGCGCGGGACCCG
                                                                                               GCGGGCTCCGGGACGGACAGAGAGGCGGGCGGGGGATGGTGCGGGGCTGCGGCTCCTGC
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GTCCCTCCCAGCGGCGCGTGA¢CGGCACTGATTTGTCCCTGGGGCGGCAGCGCGACCCG
                                                                          GCACGAGCCGGGACGGACAGAGAGGCGGGGCGGGGGATGGTGTGCGGGGTGCGGCTCCTGC
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                                                                                                                                                                                                                                /cell_type="Trabecular Bone Cells"
/lab host="SURE"
/clone libe="Normal Human Trabecular Bone Cells"
/note="Torgan: Him; Vector: pBluescript; Site 1:
Library constructed by Dr. Marian Young and Dr.
Gehron Robey (NIDCR)"
                                                                                                                                                                                                                                                                                                                                       /tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
                                                                                                                                                                                                                                                                                                                                                                          /clone="NHTBC_cn02g02"
/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                         _type="mRNA"
_xref="taxon:9606"
                                                                                                                                                                   79.5%;
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                                                                                                                                              Score 397.6; DB 9;
Pred. No. 6.9e-93;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 76 row: E column: 21
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 547)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana, Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
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   Conservative
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                                                                                      /tissue_type="pooled"
/lab_host="PH10B"
/clone_lib="MARC_2PIG"
/clone_Tet="MARC_2PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sali;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon;9823"
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                     organism="Sus scrofa"
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                  77.5%;
93.3%;
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                  Score 387.6;
Pred. No. 3e-
   Mismatches
                      3e-90;
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                                     DB 10;
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   Indels
                                   Length
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Gaps
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GGCGGGCGGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGC

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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: KODELL CONTACT IN THE PROCESS OF TOWARD TISSUE PROCUREMENT: Dr. Jim Lin, University of Iowa Tissue Procurement: Dr. Jim Lin, University of Iowa Tissue Procurement: Dr. M. Bento Soares, University Process Of The Process Of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 698)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mus musculus (house mouse)
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UI-M-GH0-ceh-c-14-0-UI.r1 NIH_BMAP_GH0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of IOWA DNA Sequencing by: Dr. M. Bento Soares, University of IOWA Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCCCTCCGCACT 435
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/tissue_type="Whole brain"
/dev stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX- Asc;
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                 /strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                               mol
                                                                                                                                                                                                                                                                          organism="Mus"
                                                                                                                                                      clone="IMAGE:6839463"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Brain Molecular Anatomy Project
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CAGCTACCCTCTGCACT
                                        ATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATAT
                                                                           ATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATAT
                                                                                                                      TTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGG
                                                                                                                                                           TTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGA 423
                                                                                                                                                                                                   GATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                  CAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Hrain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               program coordinator."
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Pred. No. 6.1e-85;
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KEYWORDS
SOURCE
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BC062938
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                                 AUTHORS
                                                                                              ORGANISM
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BC062938.1
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Klausner,R.D., Collins,F.S., Wagner,L., Shenr Altschul,S.F., Zeeberg,B., Buetow,K.H., Scha
                                                                                                                                                                           BC062938 TRNA linear Mus musculus intersectin (SH3 domain protein 1A), IMAGE:6839463), containing frame-shift errors.
                                            Mammalia; Eutheria;
1 (bases 1 to 5385)
                                                                            Eukaryota; Metazoa;
                                                                                             Mus musculus
                                                                                                             Mus musculus
                                                                                                                                                                         IMAGE: 6839463),
                                                                                                                                               GI:38566052
                                                                                                             (house mouse)
                                                                                                                                                                         containing
                                                           Chordata; Rodentia;
                                                             Craniata; Ver
Sciurognathi;
 Shenmen, C.M., Schuler, G.D., Schaefer, C.F., Bhat, N.K.,
                L.H., Derge, J.G., Shenmen, C.M., Sc
                                                             Vertebrata; I
thi; Muridae;
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                                                             Euteleostomi;
Murinae; Mus
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JOURNAL
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                     124
                                                                                  425;
                                                                                                                                        64
                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. ¢onsortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome uiowa.edu; tom-casavant@uiowa.edu Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu Bonaldo,M.F., Akabogu,I, Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Smir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                         AGAGGCGGGCGGGATGGTGCGGGCTGCGGCTCCCTCCCAGCGGCGCGTG
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/clone_lib="NIH_BMAP_GH0"
/lab_host="DH10B"
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector:|pYX-ASC"
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/clone="IMAGE:6839463"
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Pred. No. 1e-84;
0; Mismatches
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밁 Ś В Ś 뮹 Š

178

GGCTGCACTGATTTGTGTGAGGGGGGGGGGCGCGCGCACCCGGGAGATGAGGCGTCGAT

237

ORIGIN

Search completed: July 1, 2004, 13:01:15 Job time: 2663 secs

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Minimum
Maximum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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152.8	152.8	154.4	241.8	241.8	3 4 5	345	345	357	357	428	444.4	471.4	484.4	486	486	486	486	486	486	486	486	500	Score
30.6		30.9	48.4	48.4	69.0		69.0	71.4	71.4	85.6	88.9	94.3	96.9	97.2	97.2	7	97.2	97.2	97.2	97.2	97.2	100.0	י אל
967	967	6103	5144	3723	568	568	568	5738	5082	2079	3319	676	7435	5458	5195	3466	2131	2131	1676	877	877	5199	Length
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AAS31616	AA163832	AAK52332	AAZ39025	AAZ39009	ABK43814	AAS31621	AAI63919	AAZ39024	AAZ39008	AAZ34573	ABK43498	AAH08146	AAS84763	AAZ34571	AAZ34572	AA163825	AAH16578	AAK94139	AAK94611	AAK91610	AAK93179	AAZ34570	ID
Aas31616 cDNA enco		Aak52332 Human pol	Aaz39025 Mouse Ese	Aaz39009 Mouse Ese	Abk43814 DNA encod	CDNA	9	Aaz39024 Mouse Ese	Mouse	Aaz34573 Human SH3	DNA er	Aah08146 Human cDN			Aaz34572 Human SH3	Human	Human	Aak94139 Human ful	Human	0 Human	Aak93179 Human cDN	Aaz34570 Human SH3	Description

Korenberg JR,

Chen

(CEDA-) CEDARS

SINAI HEALTH SYSTEM. 98US-0082007P

P-PSDB; AAY32154.

1999-633829/54.

16-APR-1998;

This is the nucleotide sequence of full-length cDNA corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage.

The

Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.

Claim 2; Fig 5; 99pp; English.

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109	109	109	113.2	122.4	122.8	122.8	133.6	133.6	133.6	133.6	133.6	137.8	137.8	137.8	137.8	137.8	137.8	140.4	140.4	152.8	•
21.8	21.8	21.8	22.6	24.5	24.6	24.6	26.7	26.7	26.7	26.7	26.7	27.6	27.6		27.6					30.6	9
292	292	292	4447	462	982	982	4975	3593	480	480	480	2017	2017	2017	531	531	531	6014	4625	5828	967
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AAI48103	ABA67887	AAI22800	AAS02055	ACH34516	ABQ32430	ABQ32431	AAZ39027	AAZ39011	ADA08809	ABN72644	AAA69750	ADA08821	ABN72656	AAA69762	ADA08754	ABN72589	AAA69695	AAZ39026	AAZ39010	AAL47247	ABK43821
Aai48103	Aba67887	Aai22800	Aas02055	Ach34516	Abq32430	Abq32431	Aaz39027	Aaz39011	Ada08809	Abn72644	Aaa69750	Ada08821	Abn72656	Aaa69762	Ada08754	Abn72589	Aaa69695	Aaz39026	Aaz39010	Aal47247	ADK43621
Probe #16		Probe #12	_ =	Human end	Ofigonuci	Oligonuci	Mouse Ese		Human ova	Ovarian c	Human ova	Human ova	Ovarian c	Human ova	Human ova	Ovarlan c	Human ova	Mouse Ese	Mouse Ese	Allergic	DIVA effect

ALIGNMENTS

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RESULT 1
AAZ34570
SH3DlA gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; th
                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                      Human SH3D1A cDNA.
                                                                                                                                                                                                                                                                                                                                   AAZ34570 standard; cDNA; 5199 BP.
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                      01-FEB-2000
                                                                                                                                                                                                                                                                                                                    AAZ34570;
                                                                                                                                              16-APR-1999;
                                                                                                                                                                            WO9953062-A2.
                                                                                                                                                             21-OCT-1999.
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                                                                                                                                                                                                  Location/Qualifiers
208. .3642
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AAK93179
ID AAK9
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AC AAK9
XC AAK9
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DT 06-N
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention CP provides methods for the disquests and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute CP claukaemia, neural disorders, thromobocytopenia, platelet disorder on CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CP chromosome 21 with leukaemias, neural abnormality methods are CP chromosome 21 with leukaemias, neural abnormality myeloproliferative disorder, haematopoietic CP chromosome 21 with leukaemia; and treatment of a subject CP chromosome 22 with leukaemia; and treatment of a subject CP chromosome 23 with leukaemia; and treatment of a subject CP chromosome 24 with leukaemia; and treatment of a subject CP chromosome 25 with leukaemia; and treatment of a subject CP chromosome 26 prematal subject) having megakaryocytic abnormality, myeloproliferative disorder, leukaemia or neural CP chromosome 25 platelet disorder, platelet disorder, leukaemia or neural cP chromosome 26 platelet disorder, leukaemia or neural cP chromosome 27 platelet disorder, leukaemia or neural cP chromosome 28 platelet disorder, leukaemia or neural cP chromosome 29 platelet disorder, leukaemia or neural cP chromosome 20 platelet disorder, leukaemia or neural cP chromosome 21 with myeloproliferative disorder or leukaemia or neural cP chromosome 21 with myeloproliferative disorder or leukaemia or neural cP chromosome 21 with myeloproliferative disorder or leukaemia or neural cP chromosome 21 with myeloproliferative disorder or leukaemia or neural cP chromosome 21 with myeloprolifera
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Best Local Similarity
Matches 500; Conserv
                       Human cDNA clone representative
                                                                           06-NOV-2001
                                                                                                                                                                             AAK93179
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                                                                                                                                                                        standard;
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                                                                        (first entry)
                                                                                                                                                                        cDNA; 877
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Pred. No. 3e-142;
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                    sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                    SEQ ID NO: 1639
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08-JUL-1999; 99JP-00194486
11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                                                             Wakamatsu A,
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                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                              (HELI-) HELIX RES INST.
                                                                                                                                   Nishikawa T,
                                                                                                                            kawa T, Isogai T, Hayashi K, I
Sugiyama T, Nagai K, Kojima S,
                                                                                                                                  Ishii S,
                                                                                                                             Otsuki
                                                                                                                            Kawai Y;
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830 Primers useful for synthesizing WPI; 2001-524255/58. genetic manipulation. full length cDNA clones and their use

Example 11; SEQ ID NO 1639; 1380pp + Sequence Listing; English

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from

Sequence 877 BP; 208 A; 228 C; 223 G; 213 T; 0 U; 5 Other;

Length 877;

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Matches 486; Conserv
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                                                         CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATTC
                                                                                                                                                     AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC 254
                                                                                                                                                                                                                                             GGGATGGTGCGGGGCTGCCGCCTCCTGCCTCCCAGCGGCGCGCGTGAGCGGCACTGA
                                                                                                                                                                                                                                                                           CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC
                                                                                                                                                                                  TTTGTCCCTGGGGCGGCAGCGCGGACCCCGCAGATGAGGCGTCGATTAGCAAGGTAA
                                                                                                                                                                                                                               GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT
                                                                                                                                                                                                        TTTGTCCCTGGGGCGGCAGCGGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA 194
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                  97.2%; Score 486; DB 4; 100.0%; Pred. No. 2.4e-13
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RESULT 3
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Matches 486
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA 5'-end sequence,
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                                                                                                                                                                                                                                                                                                                                                                                830 Primers useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota
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                                                                                                                                                  Sequence 877
                                                                                                                                                                                                  libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent
                                                                                                                                                                                                                                                                                                                                                                   in genetic manipulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa T, !
su A, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HELIX RES INST
                                                                                                                Similarity
                                                                                                                                                                           form part of the printed specification, but was obtained at directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC 494
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                                                               SEQ
 GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
                      GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00194486.
2000JP-00118774.
2000JP-00183765.
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                                                                                                                                                    BP; 208 A; 228 C;
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na T, Nagai
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                                                                                                   0
                                                                                                               Score 486;
Pred. No.
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K, Kojima
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S, Otsuki
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T, Koga
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RESULT 4
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11-JAN-2000;
02-MAY-2000;
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P-PSDB;
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                                                                                                                                                                                                                                                          830 Primers useful for synthesizing full length cDNA clones
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                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu
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DB; AAM93676.
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2000JP-00183765
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a T, Na
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Nagai
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K, Kojima
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T, Kc
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The invention relates to primers for synthesising full length cDNA clones, 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers

Disclosure;

SEQ ID NO 3565; 1380pp +

Sequence Listing;

English

genetic

manipulation.

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AAK94139
ID AAK9
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                        08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                 Human; full length cDNA; cDNA
                                                                                                                                                                                                                                                                                                                                                                                    Human full-length
                                                                                                                             07-JUL-2000;
                                                                                                                                                                                   05-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1676 BP; 485
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2000JP-00118774.
2000JP-00183765.
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Pred. No. 3.3e-138;
                                                                                                                                                                                                                                                                                                                              $ynthesis; oligo-capping;
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(HELI-) HELIX RES INST.
                                                                                               Nishikawa T,
                                                                                          kawa T, Isogai T, Hayashi K, I
Sugiyama T, Nagai K, Kojima S,
                                                                                          Ishii S, Kawai Y;
S, Otsuki T, Koga
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830 Primers useful for synthesizing in genetic manipulation full length cDNA clones and their use

SEQ ID 2646; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly

Sequence 2131 BP; 694 A; 469 C; 526 G; 442 T; 0 U; 0 Other;

Query Match Best Local

Similarity

100.0%; 97.2%;

Length 2131;

Š 밁 S 밁 Ś 멍 Ş 밁 밁 Š Ş 멍 8 뮍 Š B Ş Matches 486; 495 432 435 372 375 312 315 192 195 132 252 255 135 72 75 GGGATGGTGTGCGGGGCTCCGGCTCCTGCCTCCCAGCGGCGCGCGTGAGCGGCACTGA GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT TGCACT 500 TGGATTCATTACTGGTGATCAAGCTAGAAACTTTTTTTTCAATCTGGGTTACCTCAACC AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC TTTGTCCCTGGGGCGGCAGCGCGGACCCGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCCAATATC CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC TTTGTCCCTGGGGCGCAGCGCGGACCCGGCCCGGAGATGAGGCGTCGATTAGCAAGGTAA GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA Conservative 0; Score 486; DB 4; L Pred. No. 3.8e-138; Mismatches Indels 0 Gaps 494 431 371 374 311 314 251 191 194 131 71

AAH16578 ID AAH1 XX

AAH16578

standard; cDNA; 2131

ΒP

492

194

393

CAATCTGGGTTACCTCAACC

633 494 573 434 513 374 453

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                                                                                                                                                                                                                                                                                                CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC chigonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in CC gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs and Specialised methods. AAH33165 to AAH13628 and CC cDNAs easily without any specialised methods. AAH30316 to AAH13628 and CC coligonucleotides, all of which are used in the exemplification of the CC coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                   Query Match
Best Local Sim
Matches 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length cDN
diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length cDNAs defined in the specification. Where a primer set comprises an oligo-dT primer and an oligo-udleotide complementary to the complementary strand of a polynucleotide which comprises one of the nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combinate oligonucleotide comprises at least 15 nucleotides; or (b) a combinate of the comprise of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sets for synthesizing polynucleotides, particularly the 5602 full-cDNAs defined in the specification, and for the detection and/or sis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELIX RES
                                                                                                                 SEQ ID
                                                                                            2131 BP;
                GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA
                                                        GGGATGGTGCGGGCTGCGGCTCCTGCGTCCCCAGCGGCGCGTGAGCGGCACTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                  691 A; 448
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LT, Wakama
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                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                           97.2%;
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                                                                                                                                                                     Score 486; DB
;; Pred. No. 3.8
0; Mismatches
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11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                         18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebroprotective; nootropic; neuroprotective; antibacterial; virucide fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory, antiulcer; vulnerary, anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss.
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24-FEB-2000;
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2000US-0184664P.
2000US-0184664P.
2000US-0186350P.
2000US-0199074P.
2000US-0199123P.
2000US-0209467P.
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2000US-0216840P.
2000US-0217487P.
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2000US-0224518P.
2000US-0225214P.
2000US-0225214P.
2000US-0225266P.
2000US-0225268P.
2000US-0225447P.
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2000US-0226759P.
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2000US-02268681P.
2000US-0226879P.
2000US-0226879P.
2000US-0226879P.
2000US-0229349P.
2000US-0229344P.

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The invention relates to human polynucleotides (AAI63803-AAI64012) and CC the encoded proteins (AAM43497-AAM4366) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (ant)agonists CC are useful in the diagnosis, treatment and prevention of: (a) cancer, CC e.g. breast and ovarian cancer and other cancers of the adrenal gland, CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or CC urogenital, (b) immune disorders e.g. Addison's disease, allergies, CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabettes mellitus, CC crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal cc and parasitic infections. Note: The sequence data for this patent did not
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01-DEC-2000
01-DEC-2000
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11-DEC-2000;
05-JAN-2001;
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P-PSDB; AAM43519.
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2000US-0251479P.
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2000US-0251856P.
2000US-0251868P.
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2000US-0251869P.
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14-AUG-2000
14-SEP-2000
01-SEP-2000
02-OCT-2000
01-NOV-2000
08-NOV-2000
08-NOV-2000

2000US-0231243P 2000US-0231244P 2000US-0231244P 2000US-0231414P 2000US-0231414P 2000US-0232080P 2000US-0232080P 2000US-0232080P 2000US-0232396P 2000US-0232396P

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2000US-0241786P.
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2000US-0241809P.
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2000US-0246475P.
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RESULT 8
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                         TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT
                                                                                            Conservative
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97.2%;

Score 486; DB 2; Li Pred. No. 5.9e-138; Mismatches

Length Indels

5195

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Gaps

194

225

254

345 314 285

465 434 405 374 134

105 74

165

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CC corresponding to a novel human SH3 gene, termed the SH3DIA gene, that CC corresponding to a novel human SH3 gene, termed the SH3DIA gene, that CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DIA gene maps to the small candidate CC region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at CC least 3 isoforms exist. The invention provides methods for the diagnosis CC and treatment of megakaryocytic abnormality, myeloproliferative disorder, CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder, acute help and disorders including brain malformations and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves, screening for a somatic alteration in the SH3DIA CC gene, monitoring the progress and adequacy of a treatment, monitoring the progress or megakaryoctyic abnormality, myeloproliferative disorder, leukaemia, hematopoietic disorder, platelet disorder, leukaemia; and cc disorder, leukaemia or neural disorder platelet disorder, platelet 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that CC contributes to the development of platelets and the pathogenesis of CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate CC region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see ARZ34570-74) suggests that at CC least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myelopyoliferative disorder, CC platelet disorder on chromosome 21, low platelets in deletion for 21, cassociation of gains in chromosome 21 with leukaemias, neural CC abnormalities, dysfunctions and disorders including brain malformations and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA CC gene; monitoring the progress of megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder, heematopoietic disorder, platelet subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia; and creatment of a subject (including a prenatal subject) having cc disorder, leukaemia or neural disorder using a nucleic acid that
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                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                          31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
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                                                                       (HYSE-) HYSEQ INC.
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2000US-00649167.
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Pred. No. 6.1e-138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
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CC complementary strand of a polynucleotide which comprises one of the 5602 CC nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence, where the complementary to a coligonucleotide comprises a 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in comparison of the 5'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, comparison and in the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC cDNAs and AAH18742 represent human cDNA sequences; AAB92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent the constant in the exemplification of the constant in the constant is the constant of the constant in the constant is the constant of the constant in the constant of the constant is constant.
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                        invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 99JP-00248036.
; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes primer sets
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ı A, Nagai K
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		roimmune disease; rheumatoid arthritis; pplasm; cardiovascular disorder; disorder; ischaemia; angiogenesis; ner's disease; AIDS; ocular disorder; ydsphagia; gastrointestinal disorder; testicular feminisation; ancer; leukaemia; neovascularisation; rder; kidney failure; blood disorder; ting; cell proliferation; skin aging; gene therapy; gene; ss.	BP. Vous system protein #78.		CACTAGCTGACATGAATAATGATGAAGAATGGATCAAGT 4	CAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATC 3	GTACGGCGGCTCGGAGGAAGAATCCCGAGCGGGCTCCGGGACAGAGAGAG
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                                                                         treating or ameliorating preservatives.
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08-NOV-2000;
The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
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and used as food
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preventing, additives or

Homo

sapiens

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Best Local S
Matches 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The
                                          megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcep
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                            lissencephaly;
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                                                                                     gene;
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                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                 CAAGGATATCAGCTACCCTCTGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAAT
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                                                                                        human;
                                                                                                                      CDNA
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                              colpocephaly;
                                                                                                                      clone
                                                                                                                                                                                                             CDNA;
                                                                                       Down's syndrome; leukaemia;
                                                                                                                                                 entry)
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capabilities,
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Pred. No. 2.
                               holoprosencephaly;
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                            diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocaphaly, Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment, monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, betweenia or neural disorder using a nucleic acid that expresses SH3DIA or its antisense nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a cDNA clone, termed clone 5, corresponding to a movel human SH3 gene, termed the SH3D1A gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3D1A gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid from the human SH\betaD1A gene and its products, useful for diagnosis and treatment of myeloproliferative disorders and leukemia.
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TCTGGATTACTGGTGAT¢AAGCTAGAAACTTTTTTTTCAATCTGGGTTACCTCAA
                                                                                                                                                                                AAAAGTAACAGAACCATGGCT¢AGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGG
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                                                              GCCATAACTGTAGAGGAAAGAĞCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATA
                                                                                                   СССАТААСТСТАСАССАЛАСАФССААССАТСАТСАССАСТТССАТАСТТТАААСССААТА
                                                                                                                                                                                                                       GATTTGTCCCTGGGGCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 12; 99pp;
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cc with Esp15 protein), vesicular trafficking and actin cytoskeleton.

C Generally (1) (or its (ant)agonists, mimerics, fragments and inactive mutants); (1) specific antibodonists, by; sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Ese1 is used to blook clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variants (Ese = EH-domain and SH3-domain regulator of endocytosis) are involved in regulation of clathrin-mediated endocytosis (as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 38-40; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Esel and 2 proteins, involved in regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998;
05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocytosis, used e.g. for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Esel full length cDNA sequence.
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99US-0118739P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                        98CA-02230201
99US-0118739P
                                                                                                                 99WO-CA000375.
                       & DEV LP
                                                                                                                                                                                                                                                                    antiviral;
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The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polymucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting CC changes in cellular function. Particularly overexpression of Esel is used CC to block clathrin-mediated endocytosis in vivo or in cell cultures, while CC (Ant)agonists of (I) is used to promote endocytosis of selected cells. CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of CC cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent cultures, by forming an Ese-Espl5 complex, then binding dynamin to the CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal correspondence represents mouse Facil. CNM semience
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection
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Sequence 5738 BP; 1556 A; 1456 C; 1613 G; 1113 T; 0 U; 0 Other;

sequence represents mouse EselL cDNA sequence

Similarity

71.4%; 85.5%;

DB 3; .2e-98;

Length

5738;

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                                          ATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATAT
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                         ATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATAT
                                                                                    TTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGG
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-216-003A-72
US-09-215-081-72
US-09-215-081-72
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US-09-216-003A-60
US-09-318-933-60
US-09-312-762A-2
US-09-312-762A-2
US-09-312-762A-3
US-08-495-737-1
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475 CA 309 CA	355 CA 189 CA 415 GA 415 GA 249 GA	95 29	atch cal s 205 175 9	ESULT 1 Sequence 5, Application US/09- Batent NO. 6468546 GENERAL INFORMATION: APPLICANT: Mitcham, Jennife: APPLICANT: Mitcham, Jennife: APPLICANT: Ning, Gordon E. APPLICANT: Ning, Gordon E. APPLICANT: Ning, Gordon E. APPLICANT: 11TLE OF INVENTION: COMPOSITITIE OF INVENTION: DIAGNOS: FILE REFERENCE: 210121.462C; CURRENT APPLICATION NUMBER: 1 CURRENT FILING DATE: 1999-01 NUMBER OF SEQ ID NOS: 393 SOFTWARE: FastSEQ for Windon LENGTH: 531 TYPE: DNA ORGANISM: Homo sapien ORGANISM: Homo sapien	
AGGATAI	ATCTGGC		ilarity Conser Conser CGTCGAT CTGAGAGG	99A-5 5, Application 6468546 1F. Mitcham, J. 1F. Mitcham, J. 1F. Algate, Parl INVENTION: D. 20 INVENTION: D. 21012 DATE: 21012 24PPLICATION NULL 24PPLICATION NULL 24PPLICATION NULL 24PPLICATION NULL 25 ID NOS: 5250 ID NOS: 525	77777777777777777777777777777777777777
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491 325	CAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAAT		GGCAGCCTGGATATCTGGGCCATAACTGTAGAGGAAAGGAAGG	19404879A EER L. IITIONS AND METHODS FOR THE SEIS OF OVARIAN CANCER 202 US/09/404,879A O9-24 dows Version 3.0	US-08-486-421-2 US-08-470-911-2 US-08-486-809-2 US-09-103-840A-2 US-09-103-840A-1 US-09-103-840A-1 US-09-144-914-3 US-09-144-914-3 US-09-144-914-3 US-08-940-086A-57 US-08-940-085A-57 US-08-940-035A-57 US-08-940-035A-57 US-08-931-05A-57 US-09-318-797-57 US-09-313-994A-4230 US-09-313-994A-4230 US-09-328-352-1885 US-09-328-352-1885 US-09-328-352-1885 US-09-674-460-1
	CACAGATATGGGCACTAGCTGACATGAATAAT 414	12 18	Length 531; Indels 0; Gaps 0; GTTTCCAACACCTTTTGGT 234	THERAPY AND	Sequence 2, Appli Sequence 3, Appli Sequence 57, Appli Sequence 57, Appl Sequence 58, Appl Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli

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FILE REFERENCE: 210121.462C1

CURRENT APPLICATION NUMBER: US/09/338,933

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 531

TYPE: DNA

ORGANISM: Homo sapien

US-09-338-933-5
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT FILLING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
                                                                          US-09-215-681-5
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US-09-215-681-5
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                                                                                         SEQ ID NO 5
LENGTH: 531
TYPE: DNA
ORGANISM: Homo
 Best Local Similarity Matches 205; Conserv
                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09215681A Patent No. 6528253
                                     Query Match
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Best Local Similarity
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APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: OVARIAN CANCER
                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version
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   Conservative
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                  27.6%;
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Score 137.8; DB 4;
Pred. No. 1.1e-33;
0; Mismatches 112;
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Pred. No. 1.1e-33;
0; Mismatches 112;
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APPLICANT: Micham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
ORGANISM: Homo sapiens
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US-09-216-003A-5
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 205;
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Best Local Similarity
       475
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   CAAGGATATCAGCTACC 491
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                                                                                                                                                                                                                        GGAGGGCCAAATATGTGGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTT
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                                           GATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAAACTCATCAAGTTAAAGTTG 308
                                                                           GATGGAAGAATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTA 474
                                                                                                                                            CAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAAT 414
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                                                                                                                 CAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAG
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CAGGCCAACAGCTGCC

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RESULT 6
US-09-338-933-72
. Sequence 72, Application US/09338933
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US-09-404-879A-72
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                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.46221
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
                                                                                    SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 72
LENGTH: 2017
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 72
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
                                    ORGANISM: Homo sapien
-09-338-933-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 27.6%;
Local Similarity 64.7%;
                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                        309
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US-09-215-681-72
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Patent No. 6528253
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Best Local
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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILLING DATE: 1998-12-17
NUMBER OF SEO ID NOS: 310
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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Pred. No. 2.3e-33;
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US-09-404-879A-60
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US-09-216-003A-72
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4620.
                                                       SEQ
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CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 72
SEQ ID NO 72
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITION
FILE REFERENCE: 210121.462
                                                                                                                                                                                                                                                                                             Sequence 60, Application US/09404879A Patent No. 6468546
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Best Local Similarity
Matches 205; Conserv
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                                                                                    FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
                                                       SOFTWARE: |
EQ ID NO 60
TYPE: DNA
ORGANISM: Homo
                                      LENGTH: 480
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                                                                         FastSEQ for Windows Version 3.0
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64.7%;
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Pred. No. 2.3e-33;
0; Mismatches 112;
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GENERAL INFORMATION:
APPLICANT: Miccham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210111.462C1
CURRENT APPLICATION UMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
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US-09-338-933-60
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 60
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 648893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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254
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                                                                                                                                                                    GGTGATCAAGCTAGAAACTTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTTAGCACAG 387
                                                                                                                                                                                                                                              GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAAGCCAATATCTGGATTCATTACT 327
                                                                                                                                                                                                                                                                                  ATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAA 73
                                                                                                                                                                                                                                                                                                            ATGGCTCAGTTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG 267
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                             GCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACC
                                                                                                                                        GGTGATCAAGCCCGTACTTTTTTCCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAA 193
                                                                                                                                                                                                             GAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTTACATAACA 133
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                                                                   ATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGACCAGCAAGAGTTCTCTATA
                                                                                                    ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGATCAAGCTAGAAACTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG 387
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                                                                                                                                                                                                                                                                                                                                                                      Score 133.6; DB 4
Pred. No. 2.2e-32;
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                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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US-09-215-681-60

Sequence 60, App. Patent No. 6528

Application US/09215681A

Patent No.

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US-09-216-003A-60
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APPLICANT: Mitcham,
APPLICANT: Frudakis,
APPLICANT: King, Gov
                                                                                                                                US-09-216-003A-60
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
PILE REFERENCE: 210121.463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                Sequence 60, Application US/09216003A Patent No. 6670463
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                                                              Matches
                                                                                             Query Match
                                                                                                                                                                                                SEQ ID NO 60
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                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOST
FILE REFERENCE: 210121.462
                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                            LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
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nes 190; Conserv
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                               208 ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG 267
                                                              190;
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                                                                               Similarity
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 ATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAA
                                                                                                                                                                                                                 PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                Frudakis,
                                                                                                                                                                                                                                                                                                                                                   Mitcham, Jennifer L.
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                  Gordon
                                                                                                                                                                                                                                                                                               COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                Tony N.
                                                                             26.7%;
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                                                          Score 133.6; DB 4
Pred. No. 2.2e-32;
0; Mismatches 94
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                                                                 Indels
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US-09-312-762A-6
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Patent No. 6552177
GENERAL INFORMATION:
                                                                                                                                           Matches 153;
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDION TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 con-
SOFTWARE: an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MIA HOROW
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3635
                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20 FEB 1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2001 Je:
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 9/2-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Friedmam, Mark M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/0 FILING DATE: 20 FEB 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
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                                                                                             ACCTTTTGGTGGAGGCTGGATATCTGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGA
 TGAGATCTTCTACACCTTATCCCCAGTGGATGGCAAGATCACAGGTGCCAACGCCAAGAA
                                TCAGCAGTTCCATAGTTTAAAGCCAATATCTGGATTCATTACTGGTGATCAAGCTAGAAA 344
                                                                    Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Mark M. Friedman c/o Anthony Castorina
2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIA HOROWITZ ET AL.
NVENTION: EH DOMAIN CONTAINING
SEQUENCES: 27
                                                                                                                                             Conservative
                                                                                                                                                          15.8%;
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                                                                                                                                                            Score 79.2; DB Pred. No. 1e-14;
                                                                                                                                         Mismatches
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                                                                                                                                                                             Length 3635;
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TOPOLOGY:
US-09-312-762A-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026
FILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,88
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word for Windows SOFTWARE: an ASCI file CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 1.44 me
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TOPOLOGY: linear
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OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                      1439 TACACACTGTCTCTCTCAACGGCAAGATCACAGGTGCTAATGCCAAGAAGGAGGAGGTGGTG
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355 CAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAAT 414
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                                                                                      CATAGTTTAAAGCCAATATCT¢GATTCATTACTGGTGATCAAGCTAGAAACTTTTTTTT 354
                                                                                                                        GGCATTGATGATGTTGAGTGGGTÄGGTTĞGCAÄĞĞÄCÄAGCCCÄCCTÄTĞÄTGÄĞATCTTC
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Pred. No. 1.4e-
0; Mismatches
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No. 1.4e-11;
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: 20 FEB 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
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CITY: Arlington
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                                                                                                                                                                                                                                                                         Local Similarity
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Friedmam, Mark M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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GATGGAAGAATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTA 474
                                   AAGTCCAAGCTGCCCAACACAGTGCTGGGGAAGATCTGGAAGTTGGCAGATGTGGACAAG
                                                                                                                                          GGCATTGATGATGTGGGTAGTTGGCAAGGACAAGCCCACCTATGATGAGATCTTC
                                                                                                                                                                                                                 GGCAGCCTGGATATCTGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTC 294
                                                                     CAATCTGGGTTACCTCAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAAT 414
                                                                                                        TACACACTGTCTCCTGTCAACGGCAAGATCACAGGTGCTAATGCCAAGAAGGAGGAGGTGG 9219
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                                                                                                                                                                                                                                                                                                                                                                                                    14707
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2001 Jefferson Davis Highway, Suite 207
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VENTION: EH DOMAIN CONTAINING GENES AND PROTEINS
EQUENCES: 27
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                                                                                                                                                                                                                                                                                                                                              linear
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Pred. No. 3.3e-11;
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Minimum
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DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
/ cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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137.8	152.8	152.8	152.8	152.8	152.8	152.8	345	345	345	345	345	444.4	486	Score
27.6	30.6	30.6	30.6	30.6	30.6	30.6	69.0	69.0	69.0	69.0	69.0	88.9	97.2	% Query Match
531	5828	967	967	967	967	967	568	568	568	568	568	3319	3466	Length
9	13	16	16	13	11	10	16	16	13	11	10	11	16	DB
US-09-884-441-5	US-10-398-885A-15	US-10-158-057-40	US-10-242-747-50	US-09-764-881-50	US-09-764-875-411	US-09-764-881-50	US-10-158-057-127	US-10-242-747-55	US-09-764-881-55	US-09-764-875-404	US-09-764-881-55	US-09-764-875-88	US-10-158-057-33	ID
Sequence 5, Appli	Sequence 15, Appi		Sequence 50, Appi	Sequence 50, Appl		ر ان	127,		Sequence 55, Appl				Sequence 33, Appl	Description

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60, 60, 60, 60, 60, 60, 60, 60, 60, 60,	Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl

ALIGNMENTS

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Sequence 33, Application US/10158057
Publication No. US20040014039A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
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                                                                                                                  Matches 486;
                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                           Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 384
                                                                                                                                                                                              LOCATION: (3465)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                             LENGTH: 3466
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (3465)
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                                                                                                                                   Local Similarity
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                                                                      15 GTACGGCGGCTCGCGAGGAAGAATCCCCGAGCGGGCTCCCGGGACGGGCGACAGAGAGACGCGGGCG
Conservative
                                                                                                                              97.2%; Score 486; DB 16; Length 3466; 100.0%; Pred. No. 1.7e-147;
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US-09-764-875-88
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; Publication No. US20040018969A1
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; ORGANISM: Homo
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids,
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Matches 445; Conserv
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LENGTH: 3319
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NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
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                                                                                                                  GGCGTCGATTAGCAAGGTAAAAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGT
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Pred. No. 6.8e-134;
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LOCATION: (562)
OTHER INFORMATION:
US-09-764-881-55
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US-09-764-881-55
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Publication No. US20030125246A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
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Best Local :
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NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
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TYPE: DNA
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LOCATION: (556)
OTHER INFORMATION:
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NAME/KEY: SITE
LOCATION: (536)
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NAME/KEY: SITE
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CAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTA
                                                                  TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
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Pred. No. 7.2e-102;
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RESULT 4
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SEQ ID NO 404
LENGTH: 568
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                                                                                                                                                                                                                                                                                                                                                                          Matches 368;
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LOCATION: (556)
OTHER INFORMATION:
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NAME/KEY: SITE
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ORGANISM: Homo sapiens
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                                                                                                                       CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT
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                          CCCTCTGCACT
                                                                            CAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTA
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o. US20040018969A1
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Pred. No. 7.2e-102;
0; Mismatches 0;
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RESULT 5 US-09-764-881-55

Sequence 55, Application US/10242747
Publication No. US20040005577A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZO7C1
CURRENT APPLICATION NUMBER: US/10/242,747
CURRENT FILING DATE: 2002-09-13

Acids, Proteins,

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US-10-242-747-55
              RESULT 6
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PTZ07
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Best Local :
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NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (536)
OTHER INFORMATION: 1
NAME/KEY: SITE
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OTHER INFORMATION:
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OTHER INFORMATION:
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368; Conserv
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Pred. No. 7.2e-102;
0; Mismatches 0;
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APPLICATION NUMBER: 09/764,881 FILING DATE: 2001-01-17 APPLICATION NUMBER: 60/179,065

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; LOCATION: (562)
; OTHER INFORMATION: n equals a,t
US-10-242-747-55
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PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR PPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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SEQ ID NO 55
LENGTH: 568
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Best Local Similarity
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ORGANISM: Homo sapiens
FEATURE:
FEATURE: misc feature
LOCATION: (481)
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NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: n equals FEATURE:
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FILING DATE: 2000-02-04
APPLICATION NUMBER: 60/214,886
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Pred. No. 7.2e-102;
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US-10-158-057-127
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NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 127
LENGTH: 568
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Best Local :
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NAME/KEY: misc_feature

TONTION: (562)
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CURRENT FILING DATE: 2002-06-12
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ORGANISM: Homo sapiens
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OTHER INFORMATION: n equals
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CCCTCTGCACT 368
                         CCCTCTGCACT 500
                                                  CAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTA
                                                                                                       CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT
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o. US20040014039A1
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Pred. No. 7.2e-102;
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RESULT 8
US-09-764-881-50
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US-09-764-875-411
Sequence 411, Application US/09764875
; Sequence No. US20040018969A1
; Publication No. US20040018969A1
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
CURRENT APPLICATION NUMBER: US/09/764,875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09764881 Publication No. US20030125246A9 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ07 CURRENT APPLICATION NUMBER: US/09/764,881 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
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LOCATION: (879)
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OTHER INFORMATION:
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LOCATION: (659)
OTHER INFORMATION:
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TYPE: DNA
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Pred. No. 7.8e-39;
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                                        Prior application data removed
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 967
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                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Protei
FILS REFERENCE: PTZ07
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (879)
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (715)
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NAME/KEY: SITE
             TYPE: DNA
ORGANISM: Homo sapiens
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; OTHER INFORMATION:
US-09-764-881-50
                                                                                                                            CURRENT APPLICATION NUMBER: US/10/242,747
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,881
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR TILING DATE: 2000-01-31
PRIOR TILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
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                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/10242747
Publication No. US20040005577A1
GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PTZ07C1
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NAME/KEY: SITE
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
                                         APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
                                                                    APPLICATION NUMBER: 60/225,758
FILING DATE: 2000-08-14
APPLICATION
             APPLICATION NUMBER: 60/217,496 FILING DATE: 2000-07-11
                                                                                                  APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
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; OTHER INFORMATION: n equals
US-10-242-747-50
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                            Matches 208;
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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OTHER INFORMATION: n equals FEATURE:
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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RESULT 12 US-10-158-057-40 ; Sequence 40, Application US/10158057 ; Publication No. US20040014039A1 ; GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILLING DATE: 2002-06-12
Prior Application removed - See File Wrap;
NUMBER OF SEQ ID NOS: 384

Proteins,

and

Antibodies

See File Wrapper

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US-10-398-885A-15
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                                                                      APPLICANT: Sugita, Yuji
APPLICANT: Hashida, Ryoi
APPLICANT: Ogasw, Kaoru
APPLICANT: Nagasu, Takes
APPLICANT: Obayashi, Mas
APPLICANT: Saito, Hirohi
APPLICANT: Takahasi, Eik
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Matches
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                                                                                                                                                                                            Sequence 15, Application US/10398885A Publication No. US20040053282A1
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                                       APPLICANT: Nagasu, Takeshi
APPLICANT: Obayashi, Masaya
APPLICANT: Saito, Hirohisa
APPLICANT: Takahasi, Eiki
TITLE OF INVENTION: Method of Testing For Allergic Diseases
FILE REFERENCE: SHIMIZU-07907
              CURRENT APPLICATION NUMBER: US/10/398,885A CURRENT FILING DATE: 2003-08-11
PRIOR
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LOCATION: (659)
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APPLICATION NUMBER: PCT/JP01/08937
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Pred. No. 7.8e-39;
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                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09884441 Patent No. US20020119158A1
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Best Local
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SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: JP 2000-314093
PRIOR FILING DATE: 2000-10-13
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
                                                                                                                                                                                                                                                                       APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                            TYPE: DNA
ORGANISM: Homo
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                    GGCGTCGATTAGCAAGGTAAAAGTAACAGAACCATGGCTCAGTTTTCCAACACCTTTTGGT
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                                                              Score 137.8; DB 9
Pred. No. 4.3e-34;
0; Mismatches 112
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APPLICANT: Mitcham, Jennifer
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Renger, Gary Rich
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
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; ORGANISM: Homo
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US-09-907-969-5
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 2101.21.46208
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 531
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Best Local Similarity
Matches 205; Conserv
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Fanger, Gary Richard
Reed, Steven G.
Vedvick, Thomas S.
Carter, Darrick
Hill, Paul
GATGGAAGAATGGATCAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTA 474
                                                                                                                                 GATAACCTCAAACCTTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCCTA 188
                                                                                                                                                                                                        GGAGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTT 128
                                                         CAGTCAGGTCTGCCGGCCCCCGGhTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAG 248
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Db 249 GATGGGAAGATGGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTG 308
Qy 475 CAAGGATATCAGCTACC 491
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Search completed: July 1, 2004, 13:09:09 Job time: 365 secs

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309

CAGGGCCAACAGCTGCC

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Minimum
Maximum
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-MODEL=frame+ pin.mode| -DEV=xlp
-MODEL=frame+ pin.mode| -DEV=xlp
-Q=(cgn2 1, USPTO, spool p/US09720934/runat 30062004 064539 13430/app query.fasta_1.1386
-Q=(cgn2 1, USPTO, spool p/US09720934/runat 30062004 064539 13430/app query.fasta_1.1386
-Q=(cgn2 1, USPTO, spool p/US09720934/runat 30062004 064539 13430/app query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0 -LOOPECT=0 -LOOPECT=0
-UNITS=bits -START=1 -END=-1 -MATRIXEND10-THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENS=0 -MAXLENS=200000000
-USER=US09720934 @CGN 1 1 7509 @runat 30062004 064539 13430 -NCPU=6 -ICPU=3
-NO MMAP -LAGREGUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOS
-NO MMAP -LAGREGUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -CONGLOS
-NO MMAP -LAGREGUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match 100.0 100.0 905.1 905.1 905.1 905.2 905.2 905.3 Length 2199 5195 1299 1676 1676 2079 2131 2131 2131 2131 2131 2131 5458 6439 7247 5287 5199 B 10 10 10 AX870076 BD150138 AF032118 BD124639 BD126208 AF468654 HSM809003 AK027846 AK074554 BD127168 BD158570 AF182198 BD264675 AR238078 AR257619 AR283665 BC038963 AF182199 AF064244 AF114487 BD205033 BD205035 BC058925 AX880753 AK075290 BD127640 BC039036 g BC020921 AB033082 AF248540 AF132481 AF132672 BD264620 BD167848 AR238023 AX366293 AF127798 AF132478 BC020921 Homo sapi BC038963 Homo sapi AF182199 Homo sapi BD167848 Method fo AF248540 Homo sapi AB033082 Homo sapi AF082198 Homo sapi AF182198 Homo sapi BD205034 Isolated AF114487 Homo sapi AF664244 Homo sapi AF525079 Mus muscu AF132478 Mus muscu AF132478 Mus muscu AF132672 Rattus no AF127798 Rattus no AK027846 Homo sapi AK074554 Homo sapi BC058925 Homo sapi BD205035 Isolated BD205033 Isolated AF064243 Homo sapi AF1174787 Homo sapi BD205034 Isolated BD127168 BD158570 AK027846 AR238078 AR257619 AR283665 AX366293 AX870076 Sequence BD150138 Primer fo AF032118 Xenopus l AX880753 AK075290 BC039036 BD124639 Description BD264620 AR238023 AF468654 Mus muscu BX648852 Homo sapi BD127640 Sequence Primer fo Homo sapi Isolated Primer fo Homo Primer Primer fo Primer Sequence Compositi Sequence Sequence Sequence Sequence sapı

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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
FT source 1. 877
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/70
PD 22-JAN-2002
PF 07-UL-2000 JP 2000253172
PF 07-UL-2000 JP 2000253172
PF 1 TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHI SHINICHI KAWAI, AI WAKANATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, SHINICHI KOJIMA,
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1 (bases 1 to 877)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Patent: JP 2002017375-A 1639 22-JAN-2002;
HELIX RESEARCH INSTITUTE
CS Homo sapiens (human)
PN JP 2002017375-A/1639
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KC
PI ISHI,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, K
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1 (bases 1 to 877)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 82 Row: 1 Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens, Similar to intersectin 1 (SH3 domain protein), IMAGE:5784342, mRNA, partial cds. BC039036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akele,K., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,K., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1299)
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC039036.1 GI:24659505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Similar to intersectin 1 (SH3 domain /protein_id="AAH39036.1" /protein_id="AAH39036.1" //db_xref="GI:7371135" //db_xref="GI:737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Uterus, leiomyosarcoma"
/clone_Tib="NIH_MGC_71"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                       LEDEQQQKKKK"
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    459.00
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                                                                             Conservative: Mismatches:
                                                 Indels:
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                                                                                                                                                                                                                                                                                          Pred. No.:
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US-09-720-934-2_COPY_15_102 (1-88) x BC039036 (1-1299)
                                                            Best Local Similarity:
Query Match:
US-09-720-934-2_COPY_15_102 (1-88)
                                                                                                           Percent Similarity:
                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer for synthesizing full-length cDNA and use Patient: JP 2002017375-A 3071 22-JAN-2002;
HELLY RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArqMetAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IleSerGlyPheIleThrGlyAspGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ProSerAlaLeuProProValMet 88
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Ota, T., Nishikawa, T., Isogai, T.,
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                                                                                                                                                                                                                                                                                                                                                                   Primer for synthesizing full-length cDNA and use thereof Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2000 JP 2000253172
TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                459.00
100.00%
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    x BD127640 (1-1676)
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                                                                  Conservative: Mismatches: Indels:
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Nagai,K., Kojima,
                                                                                                                               Length: Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nii,S., Kawai,Y.,
Otsuki,T. and
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Best Local Similarit
Query Match:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                         Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.)p, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology, Center etc.).
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Isogai, T. and Otsuki, T.
Direct Submission
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Homo sapiens cDNA FLJ90809 fis, clone Y79AA1000778,
CH Homo sapiens intersectin long form mRNA.
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Location/Qualifiers
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/clone="Y79AA1000778"
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16-APR-1998 US 60/082007
JULIE R KORENBERG,XIAO NING CHEN
JULIS/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                 /protein_id="CAE92347.1"
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                                                                                                                                                                                                           GSGISVISSTSVDQRLVEEPVLEDEQQQIEKKI,PVTFEDKKRENFERGNLELEKRRQA
LLEQQRKEQERLAQLERAEQERKERERQEGERKRQLELEKQLKQRELEQREEERRK
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QILNDQLKQVQQNSLHRDSLVTLKRALEAKELARQHLRDQLDEVEKETRSKLQEIDIF
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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ner for synthesizing full-length cDNA and use thereof FH I
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JP 2002017375-A/2599
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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(205). (2130).
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/db_xref="taxon:9606"
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OS Homo sapiens (human)
PN JP 2002191363-A/13413
PD 09-UUL-2002
PF 28-UUL-2000 JP 200028
PF TOSHIO OTA, TAKAO ISOC
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZ
PI KEIICHI NAGAI, TETSUJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 13413 09-JUL-2002;
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                            IleSerGlyPheIleThrGlyA$pGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro
                                                                                        TrpAlaI1eThrValGluGluArgAlaLysHisAspGlnGlnPheHisSerLeuLysPro
                                                                    TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
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28-JUL-2000 JP 2000280990
TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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KEIICHI NAGAI,TETSUJI OTSUKI
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JP 2002191363-A/13413
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
MEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
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Isogai, T. and Otsuki, T.
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Masuho, Y. and Kanehori, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="pLACE1"
/note="cloning vector: |
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/db_xref="taxon:9606"
/clone="PLACE1010942"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'-& 3'-end one pass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai, T., Ota, T., Nishikawa, T., Haysanı, K., UCBUKL, ..., SUGAIO, S., IShii, S., Sugaiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Sutto, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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  TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2131 bp mRNA linear sapiens cDNA FLJ90073 fis, clone HEMBA1004110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key Technology Center etc.).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /dev_stage="embryo, 10 weeks"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                            /tissue type="whole embryo, mainly
/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                    clone="HEMBA1004110"
                                                                                                                                        7.67e-53
459.00
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                                                                           x AK074554 (1-2131)
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highly similar
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RESULT 12
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC058925.1 GI:37589134
                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: ht
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22388257
                                                                                                                                                                                                info@bcgsc.bc.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://mgc.nci.nih.gov
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US-09-720-934-2_COPY_15_102 (1-88)
                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
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                                                                                   21 IleSerGlyPheIleThrGlyA$pGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro 40
41 GlnProValLeuAlaGlnIleT\daggerpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov series: IRAK Plate: 119 Row: b Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                    TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
                                                      TrpAlaIleThrValGluGluAkgAlaLysHisAspGlnGlnPheHisSerLeuLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="ITSMI protein"
/protein_id="AH58925.1"
/db_xref="GI:37589135"
/db_xref="LocusID:6453"
/db_xref="MIM:602442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="EH; Region: Eps15 homology
/db_xref="CDD:smart00027"
935. .1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAQPPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQA RNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFSIAMKLIKLKQGYQLPSALPPVM RQPVALSSAPAFGMGGIASMPPLTAVAPVPMGSIPVGMSFTLVSSVPTAAVPPLAN GAPPVLQPLPAFAHHAATLPKSSSFSRSGFGSQLNTKLQKAQSFDVASVPVAEMAVP QSSRLKKRQLENSHJKMGGHLTGDAGKTILMQSSLPQAQLASIWNLSDIDQDGKTAA EEFILAMHLIDVAMGGQPLPPVLPPEXIPPSFRRVRSGSGISVISSTSVDQRLPEEPV LEDEQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQDRECQELAQLERAEQE LEDEQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQDRECQERLAQLERAEQE
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RNRRQELLNQRNKEQEDIVVLKAKKKTLEFELEALNDKKHQLEGKLQDIRCRLTTQRQ
EIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILNDQLKQVQQNSLHRDSLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="EH; Region: Eps15 homology domain"
'db_xref="CDD:smart00027"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="LocusID:6453"
/db_xref="MIM:602442"
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BD205035
LOCUS
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Best Local Similarity:
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Leukemia and utilization thereof

Extent: UP 2002511267-A 3 16-APR-2002;
CEDARS SINAI HEALTH SYSTEM ET AL

OS Homo sapiens (human)

PN JP 2002511267-A/3

PD 16-APR-2002

PF 16-APR-1999 UP 2000543610

PF 16-APR-1998 US 60/082007

PR 16-APR-1998 US 60/082007

PI JULIE R KORENBERG,XIAO NING CHEN

PC C12015/09,A01K67/027,C07K14/47,C07K16/18,C07K19

PC G1201/68,

PC G10333/68/JA61K48/00,C12N15/00,C12N5/00

CC Isolated SH3 gene relating to myeloproliferativ
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                  41 GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp 60
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Korenberg, J.R. and Chen, X.N.
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JP 2002511267-A/3.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT 460
                                                                                          TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
                                                                                                                                                           TrpAlaIleThrValGluGluArgAlaLysHisAspGlnGlnPheHisSerLeuLysPro 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism='Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu
                               IleSerGlyPheIleThrGlyAspGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro
                                                                                                 TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA
                   CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT
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C12N15/09, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
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                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1. (bases 1 to 5287)
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AF064243
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Antonarakis, S.E.
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ipponi,M., Scott,H.S.,
                                                                                                                                                                                LEDGOQUEKKLEVIFEGEKKRENFERGNIELEKRRÖALLEQQRKEQERLAQLERAEQE
RKEREROEQERKRQLELEKQLEKORELERGNEELEKRRÖALLEQQRKEQERLAQLERAEQE
RKEREROEGERKAGULEKKRENFERGNIELEKRRÖALLEWE
RNERGELLNQRNKEGEDIVVLKAKKKTLEFELEALNUKKHQLEGKLQDIRGKLERDSLV
RIESTINKSRELERAEITHLQQQLQESQOMLGRLIPEKQILINDQLKQVQOUSLHRDSLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAPPVIQPLPAFAHPAATLEKSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVP
QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
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                                                                                                                             IRKSTSMDSGSSESÞASLKRVASÞAAKÞVVSGEEFIAMYTYESSEQGDLTFQQGDVIL
VTKKDGDWYTGTVGDKAGVFPSNYVELKDSEGSGTAGKIGSLGKKÞEIAQVIASYTAT
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/protein_id="AAC78610.1"
/db_xref="GI:3859853"
                                                      PSNYVKLTTDMDPSQQ"
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'note="encodes
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Switzerland
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domain"

Search completed: July 1, 2004, Job time : 2015.31 secs	Qy 81 ProserAlaLeuProProValMet	Qy 61 GlnValGluPheSerI Db 329 CAAGTGGAGTTTTCCA	Qy 41 GlnProValLeuAlaGlnIle 	Qy 21 IleSerGlyPheIleThrGl 	Qy 1 TrpAlaIleThrValGluGluB 	US-09-720-934-2_COPY_15_102 (1	Alignment Scores: 2.22e-52 Pred. No.: 459.00 Score: 459.00 Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 9	/note="encodes misc_feature 28433019 /note="encodes misc_feature 31103286 /note="encodes misc_feature 33263520 /note="encodes /note="encodes /note="encodes
, 16:14:04	OVALMET 88	GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu 80 	GlnProValLeuAlaGlnIle†rpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp 60 	IleSerGlyPheIleThrGlyAspGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro	leThrValGluGluÅrgAlaLysHisAspGlnGlnPheHisSerLeuLysPro 20 	(1-88) * AF064243 (1-5287)	Length: 5287 Matches: 88 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0	codes SH3 domain" 19 10 10 11 11 12 13 14 15 16 17 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Command line parameters:

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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool p/US09720934/runat_30062004_064540_13442/app_query.fasta_1.1386
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-FGAPOP=10 -YGAPPOP=10 -YGAPPOX=10 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	CB269094	RESULT 1
<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 477)</pre>	Homo sapiens	Homo sapiens (human)	EST.	CB269094.1 GI:28443679	CB269094	cDNA 5', mRNA sequence.	1008001 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens	CB269094 477 bp mRNA linear EST 20-FEB-2003		

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JOURNAL
                                                                                                                                                                                                                                                         RESULT 2
AL711737
LOCUS
                                                                                                                                                                                         ACCESSION
VERSION
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DB:
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                                      TITLE
                                                                       AUTHORS
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DKFZp686K1884 rl 686 (syhonym: hlcc3) Homo sapiens
DKFZp686K1884-5', mRNA sequence.
                 Unpublished (1999)
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 544)
                                                                                                                                    Homo sapiens
                                                                Duesterhoeft,A., Lauber, U., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                      Homo sapiens (human)
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University of Maryland
660 Redwood St, HH497, Balt
Tel: 410 706 1672
Fax: 410 706 1622
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EST analysis of human ad
Unpublished (2002)
Contact: Gong Da-Wei
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BACKWARD: AATACGACTCACTÄTAGGGCGAATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dgong@medicine.umaryland.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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             EST cluster assembly Mamm. Genome 13 (8),
                                                                                                                                                               Sus scrofa
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EST.
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246586 MARC 2PIG
BF194430
                                                             Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A.
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G.,
Quackenbush,J. and Keele,J.W.
                                        Porcine gene discovery by normalized cDNA-library sequencing
                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
22213789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKFZp68KX1884) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Locatton/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No s1 sequence available
                                                                                                                                                                                                                                                                                                                                                        ProSerAlaLeuProProValMet 88
                                                                                                                                                                                                                                                                                                                                                                                                    CAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTA
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                                                                                                       ....yuua; metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (bases 1 to 547)
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/note="Vector: pTriplEx2;
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Sus scrofa cDNA
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Site_2:

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Cho, J.,

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Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 734)

Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
EST analysis of human adipose gene expression
                                                                                                              CB269754
CB269754.1 GI:28444339
                                                                                                                                          1008661 Human
CDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 76 row: E column: 21 Seq primer: ATTTAGGTGACACTATAG.
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                                                                       Homo sapiens
                                                                                   Homo sapiens (human)
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/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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/db_xref="taxon:9823"
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660 Redwood St, HH497, I
Tel: 410 706 1672
Fax: 410 706 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGGTGGAAGAATGGAT
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BACKWARD: AATACGACTCACTATAGGGCGAATTGG
Seq primer: GTTGGTACCCGGGAATTC.
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Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 896)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                           5', mRNA sequence.
BQ941336
BQ941336.1 GI:223
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                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                    896
AGENCOURT 8741326 NIH MGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
                                                             Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                    Homo sapiens
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cDNA Library Preparation: Rubin
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/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'.
/note="Vector: lambdaTriplEx"
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/db_xref="taxon:9606"
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                                   National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                     Bukaryota; Metazoa; Chorhata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 979)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                          Homo sapiens (human)
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/db xref="taxon:9606"
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/tissue_type="large_cell_carcinoma"
/tlone_ilb="NIH_MGC_la"
/clone_ilb="NIH_MGC_la"
/clone_ilbage-resistant)
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AGENCOURT 7050803 NIH MGC 71
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Plate: LLAM13629 row: i column: 10
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGGTCGG-3' and
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Homo sapiens
                                         Homo sapiens (human)
                                                                     BC013578.1
                                                                                                                              BC013578
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                                                                                                                                                                                                                                                                                                                               GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp 60
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                                                                                                                                                                                                                                                   CAAGTGGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTA
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb. "
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
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/db_xref="taxon:9606"
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   Homo sapiens,
BC020269
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US-09-720-934-2_COPY_15_102 (1-88) x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
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Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Tissue Procurement: DCTD/DTP/Gazdar
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/clone="IMAGE:3878242"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven Jones, Jennifer Asano, Tan Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Mess, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Nichael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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CDNA Library Arrayed by The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2126)
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                                                                                                                                                                            IleSerGlyPheIleThrGlyAspGlnAlaArgAsnPhePheGlnSerGlyLeuPro 40
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GlnValGluPheSerIleAlaMptLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu 80
                                                                                                                                                                                                                                                TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Fancreas, epithelioid carcinoma"
/clone_lib="NIH_MGC_42"
/lab_host="DH1GB-R"
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db_xref="taxon:9606"
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DB:
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 01612008930
Fax: 01612360409
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Department of Biomolecular Sciences
University of Manchester Institute of
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/strain="White Leghorn, Hisex"
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PO Box
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Boardman, P.E., Sanz-Ezquerro, J., Wilson, S.A. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Corr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
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                                                                                                             /clone_lib="CSEQCHL20"
/note="organ: limbs, Vector: pBluescript II KS(+); Site 1:
/note="organ: limbs, Vector: pBluescript II KS(+)
EcoRI; Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
r-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Out pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaag]
[5'aattcttttttttcggatccggatccggatccgaaaaaaag]
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/dev_stage="36"
/lab_host="DH10B"
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/strain="White Leghorn, Hisex"
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UI-M-BHO-aja-f-07-0-UI.sl NIH BMAP M Sl M
UI-M-BHO-aja-f-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chin, H
Contact: Chin, H
National Institute of Mental Health
National Institute Room 7N-7190, 1
                                                                                                                                                                                                                                                                              Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soans be Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov
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301 443 9890
/clone="UI-M-BH0-aja-f-07-0-UI"
/dev stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone lib="NIH BMAP M S1"
/clone "Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP M S1 library is a subtracted library derived a mixture of normalized libraries from ten regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                          db_xref="taxon:10090"
                                                                                                                                                           mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                              organism="Mus musculus"
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Rodentia;
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H_BMAP_M_S1 Mus musculus
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Sciurognathi; Muridae;
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tebrata; Euteleostomi; Muridae; Murinae; Mus

Mus

EST 15-JUL-1999 cDNA clone

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Bethesda,

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                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
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ug70all.xl Soares mammary_gland_NMLMG Mus musculus
IMAGE:1547708 3' similar to TR:Q9Z0R4 Q9Z0R4 ESEIL
                                                                                                                         Possible reversed clone:
Possible reversed clone:
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Rodentia;
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                                                                                                          quality sequence stop:
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1547708"
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                                                       organism="Mus
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                                                                                                          Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyl
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., S.
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mc
Waterston,R. and Wilson,R.
The MashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      vh30f01.x1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:888505 3' similar to TR:042287 042287 INTERSECTIN. ;,
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further :
                                                                                           4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                        314 286 1800
314 286 1810
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/note="Vector: p7733p-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7773 vector. Library is normalized. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                       GI:4374931
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96.59%
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Rodentia;
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                                                                                            Louis,
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UI-M-BHO-aja-e-07-0-UI.S1 NIH BMAP M S1 F
" " GHO-aja-e-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was previously sequenced on the 5' end only, this new data is from the 3' end
          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 501)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                             AI852070
AI852070.1 GI:5495976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found High quality sequence stop: 483.
Normalization and subtraction: two approaches
                                                            Mus musculus
                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                            ProSerAlaLeuProProValMet 88
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                                                                                                                                                                                                                                                                  GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu
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/dev_stage="7 day"
/lab_host="DH10B"
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BMAP_M_S1 Mus musculus
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facilitate gene
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National Institute of Mental Health
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                                                                                                GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu
                                                                                                                                                                                                             GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp
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ProSerAlaLeuProProValMet 88
                                                                                                                                                                    /clone="UI M-BH0-aja-e-07-0-UI"
/dev_stage="27-12 days"
/lab_nost="DH10B (Life Technologies)"
/lab_nost="DH10B (Life Technologies)"
/clone lib=NIH BMAP M S1"
/clone lib=NIH BMAP M S1"
/clone lib=NIH BMAP M S1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP M S1 library is a subtracted library derived from
a mixture of normalized libraries from ten regions of the
mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of
these ten regions of the mouse brain.
TAG_TISSUE-cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUBELELUL TAG_LIBENIH_BMAP_M_S1
TAG_SEQ=GACTC"
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Post-processing: Minimum Match 0%
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-Q=/-Q=n2_1/USPTO_Spool_p/US09720934/runat_30062004_064540_13455/app_query.fasta_1.1386
-DB=ISSued_Patests_N -QFMT=fastap_-SUFFIX=rni -MINNATCH=0.1 -LODPCL=0
-LODPEXT=0-UNITS=bits -STRATT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09720934_@CGN 1 1 284_@runat_30062004_064540_13455 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NUEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPCD=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                                                                                                                      Score
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/BCCOMB.seq:*
5: /cgn2_6/ptodata/2/ina/BCTUCS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-318-933-60
US-09-215-681-60
US-09-216-003A-60
US-09-216-003A-60
US-09-404-879A-5
US-09-215-681-72
US-09-216-003A-72
US-09-216-003A-72
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                                                                                                                                                                                                                                                                                                                SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon B.
APPLICANT: Algate, Paul A.
PITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
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TYPE: DNA
ORGANISM: Homo sapien
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                       TrpAlaIleThrValGluGluArgAlaLysHisAspGlnGlnPheHisSerLeuLysPro
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/03/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
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GENERAL INFORMATION:
                                                              Sequence 60, Application Patent No. 6528253
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Patent No. 648893
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APPLICANT: Mitcham, Jennifer APPLICANT: Frudakis, Tony N. APPLICANT: King, Gordon E.
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHO
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
COMPANDER: DESCRIPTION OF COMPANDER: DESCRIPT
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CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ 1D NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA
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US-09-720-934-2_COPY_15_102 (1-88)

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US-09-216-003A-60

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RESULT 5
US-09-404-879A-5
; Sequence 5, Application US/09404879A
; Patent No. 6468546
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RESULT 6
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DB:
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Best Local Similarity:
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LENGTH: 531
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APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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                                                               ProSerAlaLeuProProValMet
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Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: Micham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION UNMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
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 Percent Similarity:
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                                                                                                                                                            NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
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                                                                                                        TYPE: DNA ORGANISM:
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TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                             LENGTH: 531
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Percent Similarity:
Best Local Similarity:
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DB:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mitcham, Jennifer L. APPLICANT: Frudakis, Tony N. APPLICANT: King, Gordon E. TITLE OF INVENTION: COMPOSITION FILE REFERENCE: 210121.462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 531
TYPE: DNA
ORGANISM: Homo
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CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
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   ProSerAlaLeuProProValMet
                                     CAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTG 323
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APPLICANT: King, Gordon E.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 72
                                                                                                                                                                                                                                                                              Sequence 72, Application Patent No. 6488931
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                                                                                                          CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
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TYPE: DNA
ORGANISM: Homo
           LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
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Query Match:
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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
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FENGTH: 2017
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Patent No. 69
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TYPE: DNA
ORGANISM: Homo s
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APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
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TYPE: DNA
ORGANISM: Homo sapiens
                 APPLICANT: Difiore, Pier P
APPLICANT: Fazioli, Francesca
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
TITLE OF INVENTION: Factor Receptor Kinase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
STREET: 620 Newport CITY: Newport Beach
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US-08-480-145-3
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Best Local Similarity:
Query Match:
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US-08-095-737-3
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                                                                               Sequence 3, Application US/084801
Patent No. 5717067
GENERAL INFORMATION:
APPLICANT: Difiore,
APPLICANT: Fazioli,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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FILING DATE: 19930722
CLASSIFICATION: 530
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Indels:
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Best Local Similarity:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095,
FILING DATE: 22-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELECHPONE: (619) 235-0550
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 3:
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
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                                                                  594 GTGGAAATCCTTGGAAGAGTTTGGGAGTTGAGTGATTTGACCACGATGGAAAGCTTGGAC
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RESULT 15 US-08-477-389-3

Sequence 3, Application US/08477389

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GENERAL INFORMATION:
APPLICANT: DiFiore, Pier P
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
TITLE OF INVENTION: Factor Receptor Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/095,737
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH060.001A
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CURRENT APPLICATION DATA:
APPLICATION UNMERE: US/08/477,389
FILING DATE: 07-JUN-1995
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HYPOTHETICAL:
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Knobbe, Martens, Olson
STREET: 620 Newport Center Drive,
CITY: Newport Beach
STATE: California
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TOPOLOGY: lin
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                      GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu 80
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Drive, Sixteenth
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Qy 81 ProSerAlaLeuProProValMet 88
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Search completed: July 1, 2004, 19:53:37 Job time: 66.6206 secs

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Maximum Match 100%
Listing first 45 summaries
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       Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_
2: /cgn2_6/ptodata/1/pubpna/US06_
3: /cgn2_6/ptodata/1/pubpna/US06_
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/cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna//US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna//US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna//US07_NEW_PUB.seq:*
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Query Match Length

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Description

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Sequence 88, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                      US-09-764-875-88
Percent Similarity:
       Score:
              Pred. No.:
                     Alignment Scores:
                                   US-09-764-875-88
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                                                                SOFTWARE: Pa
                                          LENGTH: 3319
TYPE: DNA
ORGANISM: Homo
                                                                               Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1249
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16 US-10-158-057-33

10 US-09-764-881-55

11 US-09-764-875-404

13 US-09-764-881-55

16 US-10-242-747-55

16 US-10-158-057-127

13 US-10-398-885A-15

9 US-09-884-441-60
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US-10-027-632-290824
US-10-027-632-290824
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US-10-029-386-25205
Conservative:
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Sequence 60, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 72, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 21778, A
Sequence 50, Appl
Sequence 10751, A
Sequence 21773, A
Sequence 19751, A
Sequence 19751, A
Sequence 4631, Ap
Sequence 4631, Ap
Sequence 4631, Ap
Sequence 15796,
Sequence 165796,
Sequence 165797,
Sequence 165797,
Sequence 165797,
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Sequence 55, Appl
Sequence 404, App
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 17, App
Sequence 17, Appl
Sequence 16, Appl
Sequence 60, Appl
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Sequence 354, App
Sequence 3, Appli
Sequence 290824,
Sequence 290824,
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Sequence 25205,
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Protein
FILE REFERENCE: PIZO5C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior Application removed - See
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
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Publication No. US20040014039A1
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NAME/KEY: misc_feature
LOCATION: (3465)
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NAME/KEY: misc feature
LOCATION: (3194)
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US-09-764-881-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZO7
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - refer to NUMBER OF SEQ ID NOS: 192
                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (562)
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LOCATION: (556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (536)
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Publication No. US20040018969A1
GENERAL INFORMATION:
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SEQ ID NO 404
LENGTH: 568
                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
                                                                                                                    Sequence 55, Ap
Publication No.
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
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19-764-875-404
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LOCATION: (536)
OTHER INFORMATION:
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                                                                                                                    Application US/09764881
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                          PRIOR APPLICATION NUMBER: 09/764,881
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-07-11
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Publication No.
                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/242,747
CURRENT FILING DATE: 2002-09-13
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14
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No. US20040005577A1
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Query Match:
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            Sequence 127, Application US/10158057
Publication WS. US20040014039A1
GEMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
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LENGTH: 568
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PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 192
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LOCATION: (481)
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FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225 447
FILING DATE: 2000-08-14
   Application
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                                                                                                                                                                                                                        Sequence 15, Application US/10398885A
Publication No. US20040053282A1
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 127
LENGTH: 568
APPLICANT: Takahasi, Eiki
TITLE OF INVENTION: Method of Testing For Allergic Diseases
FILE REPERENCE: SHIMIZU-07907
CURRENT APPLICATION NUMBER: US/10/398,885A
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/JP01/08937
PRIOR APPLICATION NUMBER: JP 2000-314093
                                                                                                                                                               APPLICANT: Sugita, Yuji
APPLICANT: Hashida, Ry
APPLICANT: Ogawa, Kaor
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APPLICANT:
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NAME/KEY: misc feature
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Obayashi, Masaya
Saito, Hirohisa
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US-10-398-885A-15
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
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SEQ ID NO 15
LENGTH: 5828
                                                                                                    LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapien
:-09-884-441-60
                                                                                                                                                                                                                       APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
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NUMBER OF SEQ ID NOS: 16
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NAME/KEY: CDS
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US-09-907-969-60
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-60
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CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSEQ for Windows Version
176 GCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGAAGATGGAC 235
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                             GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp 60
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Fanger, Gary Richard
Reed, Steven G.
Vedvick, Thomas S.
Carter, Darrick
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; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo s
US-09-827-271-60
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US-10-198-053-60
US-10-198-053-60
; Sequence 60, Application US/10198053
; Publication No. US20030124140A1
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 60
                                                                APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6
CURRENT FILLING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
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; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo s
US-10-198-053-60
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5.4
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Patent No. US20020119158A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      LENGTH: 531
TYPE: DNA
ORGANISM: Homo &
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; ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 531
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C8
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CCTGTAGTCCTCCCTCCTATCATG 347
                                                                                GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu 80
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Carter, Darrick
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Sequence 5, Application US/09827271

Publication No. US20030165504A1

GENERAL INFORMATION:

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C6

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5
Search completed: July 1, Job time: 275.977 secs
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo
US-09-827-271-5
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US-09-827-271-5
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-DB=M Geneseq 29Jan04 -QFMT=fastap -SUFFTX=TNG -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US09720934 @CGN 1 1 1596 @runat 30062004 064539 13422 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARM TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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(c) 1993 - 2004 Compugen Ltd
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                    AAK93179
AAK91610
AAK94611
AAZ34573
AAK94139
AAH16578
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Aak91610 Human cDN
Aak94611 Human cDN
Aak94611 Human cDN
Aaz34573 Human SH3
Aak94139 Human full
Aah16578 Human cDN
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ALIGNMENTS

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RESULT 1
AAK93179
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11-JAN-2000;
02-MAY-2000;
WPI; 2001-524255/58.
                                         Ota T,
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                                                                                                                                                                                                                                                                                                      Human cDNA clone representative sequence,
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                                                                                                                                                                                                                                                                                                                                                                                              AAK93179 standard; cDNA; 877 BP.
                                                                                                                                                          07-JUL-2000; 2000EP-00114089
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                                                                      (HELI-) HELIX RES INST.
                                         Nishikawa T,
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                                                                                                 99JP-00194486.
2000JP-00118774.
2000JP-00183765.
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                         Sugiyama
                         Isogai T,
a T, Nagai
                           Hayashi K,
K, Kojima
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                         Ishii S,
S, Otsuki
                           Kawai Y;
T, Koga
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830 Primers useful for synthesizing full length cDNA clones and their use

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                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                        Human; full length
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Score:

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Alignment
                                                           The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                Sequence 877 BP; 208 A; 228 C; 223
                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                              830 Primers useful for
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-524255/58.
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K, Kojima
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RESULT 3
AAK94611
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DB Huma
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KW Huma
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CS Homo
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PN EP11 Ś 밁 Ś Ś 밁 Ś В 밁 B Ş Percent Similarity: Best Local Similarity: US-09-720-934-2_COPY_15_102 (1-88) x AAK91610 (1-877) Query Match: AAK94611; AAK94611 standard; cDNA; 1676 247 427 367 307 61 41 81 21 IleSerGlyPheIleThrGlyAspGlnAlaArgAsnPhePhePheGlnSerGlyLeuPro ProSerAlaLeuProProValMet 88 GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp 60 TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCA TrpAlalleThrValGluGluArgAlaLysHisAspGlnGlnDheHisSerLeuLysPro CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT 100.00% 100.00% 100.00% 뫈 Gaps: Indels: Mismatches: Conservative: 877 88 0 80 486 306 366 40 20

EP1130094-A2 Homo sapiens Human; full length cDNA; cDNA synthesis; oligo-capping; ss

Human cDNA, 07-NOV-2001

SEQ ID

NO:

3565

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RESULT 4
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                                                                                                                                                                                     CAACCTGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGAT
                                                                                                                                                                                                   GlnProValLeuAlaGlnIleTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp
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                                                                                                     ProSerAlaLeuProProValMet
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K, Kojima
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Matches:
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                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                    CC corresponding to a novel human SH3 gene, termed the SH3DIA gene, that CC contributes to the development of platelets and the pathogenesis of CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DIA gene maps to the small candidate CC region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at CC least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC abnormalities, dysfunctions and disorders including brain malformations and colpocephaly, Methods are also provided for: suppressing cells unable CC and corresponding cognitive dysfunctions, microcephaly, liseencephaly, and colpocephaly Methods are also provided for: suppressing cells unable CC to regulate themselves; screening for a somatic alteration in the SH3DIA CC gene; monitoring the progress and adequacy of a treatment, monitoring CC disorder, haematopoietic disorder, platelet disorder or leukaemia; and createner of a subject (including a preparation between the set of the subject of treatment of a subject (including a preparation between a subject of a treatment and the set of the set of the subject of the sub
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                                                                                                                                                                                                                          Sequence 2079
                                                                                                                                                                                                                                                                    treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, plateled disorder, leukaemia or neural disorder using a nucleic acid that expresses SH3DlA or its antisense nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a cDNA clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 12; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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1 TrpAlaIleThrValGluGluArgAlaLysHisAspGlnGlnPheHisSerLeuLysPro

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Alignment Scores: Pred. No.:
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11-JAN-2000;
02-MAY-2000;
                                                             The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                               Sequence 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA
                                                                                                                                                                                                  Claim
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DB; AAM93229.
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2000JP-00183765.
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na T, Nagai
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K, Kojima
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Length:
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S, Otsuki
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Percent Similarity:
Best Local Similarity
Query Match:
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RESULT 6
AAH162
AAH163
AC AAH1
XX AAH16
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 length cDNAs defined in the specification, and for the detection and diagnosis of the abnormality of the proteins encoded by the full-length specification.
                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                      Sugiyama T,
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2000JP-00183767.
2000JP-00241899.
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99JP-00300253.
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A, Nagai K,
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Otsuki
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full-length
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary to the

Claim

в<u>,</u>

SEQ

ID NO 15658; 2537pp +

Sequence Listing; English

nucleotide sequences defined in the specification,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH1872 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                              hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's Gisease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
                                                              endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therany: gene. of
                         Homo sapiens
                                                                                                                                                                                                                                                                  Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK43498
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                                                                                                                                                                                                                                                                                                             DNA encoding novel central nervous system protein #78.
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabete; and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. monallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM43497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer,
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Indels: Gaps: Conservative: Mismatches:

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Sequence 5195 BP; 1592 A; 1148 C; 1237 G;

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Corresponding to a novel human SH3 gene, termed the SH3DIA gene, that Contributes to the development of platelets and the pathogenesis of Cleukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different CC region for low platelets on chromosome 21. Sequencing of 5 different CC least 3 isoforms exist. The invention provides methods for the diagnosis CC and treatment of megakaryocytic abnormality, myeloproliferative disorder, CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder on chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3D1A CC gene; monitoring the progress and adequacy of a treatment; monitoring CC disorder, haematopoietic disorder, platelet disorder or leukaemia; and CC treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet cdisorder, leukaemia or neural disorder using a nucleic acid that cC expresses SH3D1A or its antisense nucleic acid
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                    This is the nucleotide sequence of full-length cDNA corresponding to novel human SH3 gene, termed the SH3DLA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. SH3DLA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic absorbatic methods for the diagnosis and treatment of megakaryocytic
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holoprosencephaly; diagnosis; therapy;
  disorder,
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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Method also provided for: suppressing cells unable to regulate themselves;
                                                                                                                                                       megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopojetic disorder; cognitive dysfunction; microcep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia, neural disorders, thromobocytopenia, platelet disorder chromosome 21, low platelets in deletion for 21, association of gachromosome 21 with leukaemias, neural abnormalities, dysfunctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder using nucleic acid
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                                                                                                                                                                                                                                                                                                            standard;
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of gains
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This is the nucleotide sequence of full-length cDNA (clone 21)
CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that
CC contributes to the development of platelets and the pathogenesis of
CC leukaemias, both in general and in particular those involving the
CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate
CC region for low platelets on chromosome 21. Sequencing of 5 different
CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at
CC least 3 isoforms exist. The invention provides methods for the diagnosis
CC and treatment of megakaryocytic abnormality, myeloproliferative disorder,
CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia,
CC platelet disorder on chromosome 21 to platelet in deletion for 21,
CC association of gains in chromosome 21 with leukaemias, neural
CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly,
CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly,
CC and corresponding the progress and adequacy of a treatment; monitoring
CC tumour risk progress or megakaryoctyic abnormality, myeloproliferative
CC disorder, haematopoietic disorder, platelet disorder or leukaemia; and
CC megakaryocytic abnormality, myeloproliferative disorder, leukaemia or neural disorder using a nucleic acid that
CC expresses SH3D1A or its antisense nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                        TGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) CC sequences. (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCE) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed used (CC genes. (I) is useful in gene therapy techniques to restore normal (CC activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food (CC supplement. (II) and its binding partners are useful in medical imaging (CC involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in consists, gene mapping, identification of mutations of the protein consists or other traits of severes biodiversity (CC consists) and (CC consists) are separated by the protein consists of the protein consist
                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                            Sequence 7435 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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2000US-00649167.
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     The present sequence encodes mouse Esel. The present invention CC specifically describes mammalian Esel and 2 proteins (I) and their splice CC variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) CC are involved in regulation of clathrin-mediated endocytosis (as a complex CC with Espl5 protein), vesicular trafficking and actin cytoskeleton. (CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab), sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of CC (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral
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        New nucleic acid encoding Ese1 and 2 proteins, involved in regulation endocytosis, used e.g. for treating cancer or preventing viral infecti
                                         P-PSDB;
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                                                                           Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ39008 (1-5082)
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          corregulation of calculations (1) are involved in regulation of clathrin-
commediated endocytosis (as a complex with Esp15 protein), vesicular
contrafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists,
commetics, fragments and inactive mutants); (I)-specific antibodies (Ab);
composed to treat diseases associated with undesirable endocytosis and resulting
composed in cellular function. Particularly overexpression of Esel is used
composed to treat diseases associated with undesirable endocytosis and resulting
composed in cellular function. Particularly overexpression of Esel is used
composed to block clathrin-mediated endocytosis in vivo or in cell cultures, while
composits of (I) or Ab are used to suppress abnormal proliferation of
composits of (I) or Ab are used to suppress abnormal proliferation of
composits of compounds (also inactive Ese mutants) can be used to prevent
composition. Endocytosis may also be regulated, in vivo or in cell
composition of Ese-Esp15 complex, then binding dynamin to the
composition of migration; viral infection; or abnormal
composition or migration; viral infection; or abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5144 BP; 1447 A; 1298 C; 1415 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention specifically describes mammalian Esel proteins (I) and their splice variants (Ese st EH-domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Ese1 and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1998;
05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents mouse Esell coding sequence
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                                                                            GlnValGluPheSerIleAlaMetLysLeuIleLysLeuLysLeuGlnGlyTyrGlnLeu
                                                                                                                                                  GlnProValLeuAlaGlnI1eTrpAlaLeuAlaAspMetAsnAsnAspGlyArgMetAsp
                                                                                                                                                                                                    ProSerAlaLeuProProValMet
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                                                                                                                                                                                                                                                                                              TrpAlaIleThrValGluGluArgAlaLysHisAspGlnGlnPheHisSerLeuLysPro
                                                        CAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTC
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99US-0118739P.
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SH3-domain
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Db 283 CCCTCCACACTTCCCCCTGTCATG 306
Search completed: July 1, 2004, 13:31:27
Job time: 278.625 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 _/USPT0 spool p/US09720934/runat _30062004_064539_13430/app_query.fasta_1.1386
-DB=GenEmbl -OFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITMT=bto -NORM=ext -NEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09720934_@CGN 1_7509_@runat 30062004_064539_13430 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
   GenEmbl:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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30: em htg_inv:*
31: em htg_inv:*
32: em htg_other:*
33: em htg_other:*
34: em htg_pin:*
35: em htg_pin:*
36: em htg_vrt:*
37: em htg_vrt:*
39: em htgo hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

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                        Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Gonsortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 82 Row: 1 Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc mgc@nhgrilnih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCQ
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1299)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-NOV-2002) Gene Collection (MGC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                              /product="similar to intersectin 1 (SH3 domain protein)"
/protein_id="AMH39036.1"
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RNFFFGSGLPQPVLAQLWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSALPPVM
KQQPVAISSAPAFGMGGTASWPPLTAUVAPVPMSSIPVVGMSPTLVSSVTPTAAVPPAN
KQQPVAISSAPAFGMGTASWPPLTAUVAPVPMSSIPVAGSFDVASVPPVAEWAVP
GAPPVIQPLPAFAHFAATLPKSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVP
                                                                                                                                                                                         QSSRLKYRQLFNSHÜKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPV
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/clone_lib="NIH_MGC_71"
/lab hoct-"punds"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                        note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE: 5784342"
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                                                              Percent Similarity:
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OS Homo sapiens (human)
PN JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 200025
PI TOSHIO OTA, TETSUO NIS
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SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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Primer for synthesizing full-length cDNA and Patent: JP 2002017375-A 3071 22-JAN-2002;
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BD127640.1 GI:23222585
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Ota,T., Nishikawa,T., Isogai,T.,
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Primer for synthesizing
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TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                  Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Beconomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'-& 3'-end one pass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Sugiyama,T., Saito,K., Yamamoto,J., Makamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
                                                                                                                                                                                                                                                                                                                     sequencing and clone selection: Helix Research Institute (supported
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
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Isogai, T. and Otsuki, T.
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Mammalia; Eutheria; Primates;
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Location/Qualifiers
                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                         /note="cloning
                                                                                                                                            /cell_type="retinoblastoma"
/clone_lib="Y79AA1"
                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="Y79AA1000778"
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Isolated SH3 gene relating to myeloproliferative leukemia and utilization thereof Patent: JP 2002511267-A 4 16-APR-2002;
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16-APR-1998 US 60/082007
JULIE R KORENBERG, XIAO NING CHEN
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and
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mol_type="unassigned DNA"

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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN UP 2002017375-A/2599
PD 20-JAN-2002
PD 22-JAN-2000 JP 2000253172
PD 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2131)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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JP 2002017375-A/2599.
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TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                     TGGGCTGTTCCTCAGTCATCAAGACTGAAATACAGGCAATTATTCAATAGTCATGACAAA
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KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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and Otsuki, T.
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21 ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
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US-09-720-934-2_COPY_215_310 (1-96)
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukaryota; Mutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Search Institute (supported by Japan Key Technology Center etc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito, K., Yamamoto, J., Wa
Masuho, Y. and Kanehori, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK027846 2131 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ14940 fis, clone PLACE1010942, highly similar to Homo sapiens intersectin long isoform (ITSN) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Department of Virology, Institute of Medical Science,
University of Tokyo.
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Isogai, T. and Otsuki, T.
Direct Submission
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Nishikawa,T., Nagai,K., Sugamo,S., Ishibashi,T., Fujimori,K.,
Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishil,S., Kawai,
Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K.,
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AK027846
                            TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20
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                                                                                                                                                                                                                                                                                                                                                                                                       /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta"
/clone_lib="PLACE1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.)jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Conter; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
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Eutheria;
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mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                        dev_stage="embryo, 10 weeks"
note="cloning vector: pME18S
                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
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Primates;
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, J., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, J., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1027
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Homo sapiens intersectin 1 (SH3
IMAGE:4443129), partial cds.
BC058925
                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                        Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran (
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A.
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Mammalia;
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                                                                                      info@bcgsc.bc.ca
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Primates;
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US-09-720-934-2_COPY_215_310 (1-96) x BC058925 (1-2199)
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DB:
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998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAQFPTPEGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQA RNFFPGSGLPQPVLAQIWALADMNNOGRMDQVEFSIAMKLIKLKJQGYQLESALPPVM KQQPVAISSAPAFGMGIASMPPLTAVAPVPMGSIPVGMSPTJASVPTAAVPPLAN GAPPVIQFAPAFGMGIASMPPLTAVAPVPMGSIPVGMSPTJASVPTAAVPPLAN GAPPVIQFAPAFAPAFATLPKSSSFSRSGFGSQLNTKLQKAQSFDVASVPVAEMAVP QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMGSSLPQAQLASIWNLSDIDQDGKLTA EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPPVLPEYILPESTLPEGREERRKEAGERSEGREAQLERAEQE EKERERQEBERKGQLEKKLPVTFEDKKRENELERQREERRKAALLEQQKEGGSELAQLERAEQE RKERERQEBERKGQLEKKQLEKQLEKQREEGRELEALNDKKHQLEGKLQDIRCRUTTQRQ EISSTWKSREERREAGEDIVVLKAKKKTLEFELEALNDKKHQLEGKLQDIRCRUTTQRQ EISSTWKSREERREAGEDIVVLKAKKKTLEFELEALNDKKHQLEGKLQDOIRCRUTTQRQ EISSTWKSREERREAGETHLQQQLQESQQMLGRILFEKGILNDQLKQVQQNSLHRDSLV
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/db xref="CDD:smart00027"
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MEAERLKKKK"
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/db_xref="MIM:602442"
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/db_xref="GI:37589135"
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/db_xref="LocusID:6453"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="ITSN1"
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mol_type="mRNA"
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_lib="NIH_MGC_90"
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Pred. No.: Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 3723)
Sengar, A.S., Wang, W., Bishay, J., Cohen, S. and Egan, S.E. The EH and SH3 domain Ese proteins regulate endocytosis by linking
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Mus musculus Esel protein mRNA,
AF132478
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EMBO J. 18 (5), 1159.
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                                                                                                                                                                                                                                                                                                                                KQQPVAISSAPAFGIGGIASMPPLTAVAPVPMGSIPVVGMSPPLVŠSVPPAAVPPLAN
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                                                                                                                                                                                                                                                                               SEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLERAEQER
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                               Submitted (02-MAR-1999) Center for Basic Neuroscience and HHMI, Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX
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Okamoto,M., Schoch,S. and
Direct Submission
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J. Biol. Chem. 274 (26), 18446-18454 (1999)
99303609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHSH1/intersectin, a protein that contains EH and SH3 doma binds to dynamin and SNAP-25. A protein connection between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okamoto, M., Schoch, S. and
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Mammalia; Eutheria;
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Rodentia;
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ORIGIN

RESULT 13 AF127798 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	2 2 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	US-09-720-934 QY 1 Db 683 QY 21 Db 743	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:
AF127798 Rattus norvegicus EH- and complete cds. AF127798 AF127798 AF127798 AF1277981 I GI:4835852 Rattus norvegicus (Norway Rattus norvegicus Eukaryota; Metazoa; Chorda Mammalia; Eutheria; Rodent 1 (bases 1 to 4025) Okamoto, M., Schoch, S. and EHSH1/intersectin, a prote binds to dynamin and SNAP-exocytosis and endocytosis of the condition of the conditio	41 ProGlnAlaGlnLeuAlaSe:	7-2- 7-2-	Scores: 3.9e-50 501.00 milarity: 100.00% Similarity: 100.00% h: 100.00% h: 100.00%
4025 bp mRNA linear ROD 28-JUN-1999 H- and SH3-domain containing protein EHSH1 mRNA, 1552 Vorway rat) Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; S. and Sudhof,T.C. a protein that contains EH and SH3 domains and SNAP-25. A protein connection between Cytosis? (26), 18446-18454 (1999) S. and Sudhof,T.C. 1999) Center for Basic Neuroscience and HHMI, 1 Center, 5323 Harry Hines Blvd., Dallas, TX	ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60	2_COPY_215_310 (1-96) x AF132672 (1-3812) TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20	Length: 3812 Matches: 96 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                      743 ACCATGAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTA
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                                                                                                                                                                                                                                                                                                                                                              803
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                    Homo
                                                                                Homo sapiens mRNA; cDNA
BX538175
                                                              BX538175.1
                                                                                                                        HSM806384
                                                                                                                                                                                                                       LeuProProValLeuProProGluTyrIleProProSerPheArgArg
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    sapiens
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NARGELLTÖRNKOGRGI VULKARRKTILEFELBALNOKKHÖLEGKLÖDIR ORLAMORG
IESTIKSRELRI AEITHLÖQÖLGESQÖNLÖGRI PERGLISÖDLKÖVÇÖNSLHADSILT
LKRALEAKELARGÖLREGEDEVEKETERKLÖBI DVENNÖLKELBEIHSKÖÖLÖKÖRSI
EAERLKÖKEGERKSLELEKÖKEEGÖRRVÖERDKÖMÇEHVÖQEEQÖRPKKPHEEDKLKR
EDSVUKKKEABERAKPEVÖDKÖSRLEHHHÖEPAKPAQAPMITTEKÖPLTI SAÖESAKVV
YYBALYPESERSHDEITI ÖPGDI VMVKGEMUDESÖTREMFENNMADESSTYMPS
EKI PENEI PTPAKPVTDLTSAPAPKLALRETPAPLPVTSEBESTTPNNMADESSTYMPS
STNEKKPETDMUTMAAÖPSLTVPSAGÖLRÖRSAFTPATATGSSPSPVLGÖGEKVEGLÖ
AQALYPMRAKKONHLNENKSDVI TVLEÖÖDNMAPGEVÖGOGMEPKSHENDVIVTVK
KDGDMWTGTVGETSGVEPSNYVRLKDSEGSGTAGKTGSLEKKPEI AÖVIASYTATGPE
ÖLTLAPGÖLLLI KKNAPGGMABGELÖARGKKRÖLGMFPANVYKLLSPGTSKI TPTELP
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KQQPAAISSAPAFGIGGMAGMPPLTAVAPVPMGSIPVVGMSPELVSSVPQAAVPPLAN
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMGSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPEYIPSFERVRSGSGMSVISSSSADORCLPEPES
SEDEQQVEKKLPVTFBDKKRENFERGNLELEKERQALLEQQRKEQERLAQLERAEQER
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                                                                                                 DKFZp686J17173 (from clone DKFZp686J17173)
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                                                                                                                      4321 bp
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270 ACTATGAGTGGACACTTAACAGGTCCCCAAGCAAGAACTATTCTTATGCAGTCAAGTTTA
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US-09-720-934-2_COPY_215_310 (1-96)
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Best Local Similarity:
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21 ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu
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Clone from S. Wiemann, Molecular Genome Analysis, German Caronarch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                            1 TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys
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This clone (DKFZp686J17173) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fobo,G., Han,M. and Wiemann,S.
                                                                               TGGGCTGTTCCTCAGTCATCAAGACTGAAATACAGGCAATTATTCAATAGTCATGACAAA
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PSFRRWRSGGISVISSTSVDQRLPEEFVLEDBQQQLEKKLPVTFEDKKRENFERGNL
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4289
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QERDKQMLEHVQQEDEHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLGRLFHQ
HQEPAKPAVQAPMSTAEKGPLT I SAQENVKVVYYRALYP FESRSHDEI TI QPGD I VMV
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/note="intersectin long isoform, N-terminus truncated,
/ifferentially spliced"
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/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="CAD98050.1"
/db_xref="GI:31874621"
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/db_xref="taxon:9606"
/map="21q22.11"
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|mol_type="mRNA"
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Research/Developmental Biology, The Hosp
Toronto, ON M5G-1X8,
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Mus musculus EselL protein ma
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Location/Qualifiers
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Sengar,A.S., Wang,W., Cohen,S., Bishay,J. and Egan,S.E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 5145)
Sengar, A.S., Wang, W., Bishay, J., Cohen, S. and Egan, S.E.
The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Egs15
EMBO J. 18 (5), 1159-1171 (1999)
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                                                                                                                               NRRQEĹLÑQRNKĒQÞĠTTVĪLKAŘRKTLEFELBALNDKKHQLEGKLQDIRCRLATQRQE
IESTMKSRELRIAEITHLQQOLQESQQMLGRLI PEKQILSDQLKQVQONSLHRDSLLT
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MWTGTVGDKSGVFÞSNVVRLKDSEGSGTAGKTGSIGKKPEIAQVIASYAATGÞEQLITL
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TTDMDPSQQWCSDLHLLDMLTPTERKRQGYIHELIVTEENYVNDLQLVTEIFQKPLTE
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Biology, The Hospital for Sick Children,
nto, ON M5G-1XB, Canada
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ORIGIN Scores:

Percent Similarity:
Best Local Similarity:
Query Match: Score: Alignment No.: 5.41e-50 501.00 100.00% 100.00% 100.00% 10 Length:
Matches:
Conservative:
Mismatches:
Indels:

В Ś ₽ Š 밁

US-09-720-934-2_COPY_215_310 (1-96) x AF132481 (1-5145) Š

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В 뫄 S 643 703 41 TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys ACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTA ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 762 40 702

밁 Ś 뫄 Ś 823 763 61 CCCCAGGCTCAGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTC ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60 ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro 80

Search completed: July 1, 2004, Job time: 2196.79 secs 16:14:11

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Minimum
Maximum
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aah19248 Human sec		43	192 Murine	9	484	Ada08754 Human ova	Abn72589 Ovarian c		Ada08809 Human ova	Abn72644 Ovarian c		Aah15260 Human cDN	Aah03435 Human cDN		Abl01995 Drosophil		CDN	Aai63826 Human pol	Human	Aak52332 Human pol	247 Allergic	02055	9026 Mous	9027 Mouse	0 Mouse	9011 Mouse	8821 Human	Vī	762	4763 DNA e	3825 Hum	3498	000	9024	4571 Human	4570 Human	

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ALIGNMENTS

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RESULT 1
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11-JAN-2000;
02-MAY-2000;
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           WPI; 2001-524255/58
                                                                                                                                                                                      05-SEP-2001.
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                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                                                             Human cDNA,
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P-PSDB; AAM93676
                                       Wakamatsu
                                                  Ota T,
                                                                                                                                                          07-JUL-2000; 2000EP-00114089
                                                                           (HELI-) HELIX RES INST.
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                                                  Nishikawa T,
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2000JP-00118774.
2000JP-00183765.
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                                     Sugiyama
                                     Isogai T,
a T, Nagai
                                       Hayashi K, I
K, Kojima S,
                                       Ishii S,
S, Otsuki
                                       Kawai
T, K
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Koga H;
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                                                                                                                                                                                                                    SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abhormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
      W09953062-A2
                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a cDNA clone, termed clone 5, corresponding to a novel human SH3 gene, termed the SH3D1A gene, contributes to the development of platelets and the pathogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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LeuProProValLeuProProGluTyrIleProProSerPheArgArg
                                                                                 ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro 80
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                                                             ACAGCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA
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                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                   The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing
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{\tt ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu}
                                                 ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
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Nagai
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K, Kojima
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                  sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13638 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13632 to AAH13332 represent cligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000; 2000JP-00118776
02-MAY-2000; 2000JP-00183767
09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA sequence SEQ ID NO:15658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH16578
                                                                                                                                                                                                                                                                                                                                                                                                        of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length cDNAs defined in the specification. Where a primer set of an oligo-dT primer and an oligonucleotide complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sets for synthesizing polynucleotides, particularly the 5602 full cDNAs defined in the specification, and for the detection and/or sis of the abnormality of the proteins encoded by the full-length
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, Sugiyama
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T, Wakamatsu
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A, Nagai K,
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 The present sequence encodes mouse Esel. I specifically describes mammalian Esel and
                                                      New nucleic acid encoding Esel endocytosis, used e.g. for trea
                                                                                                                                                                  27-APR-1998;
05-FEB-1999;
                                                                                                                                                                                                                                                                                   Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                               Claim 6; Page 40-42; 99pp; English.
                                                                                                  WPI; 2000-052802/04.
                                                                                                                                                                                                                      04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant) agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding dynamin to complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission
                                                                                                                                                      EH-domain and SH3-domain regulator of endocytosis;
                                                                                                                                                                        Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection;
                                                                                                                                                                                                                                 Mouse Esel full length cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (() variants (Ese = EH-domain and SH3-domain regulator of endocytosis (as a compare involved in regulation of clathrin-mediated endocytosis (as a compare the control of trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive.
                                                                                               Mus sp
                                                                                                                                    antiproliferative; antiviral; ss.
                                                                                                                                                                                                                                                                          28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                     AAZ39008 standard; cDNA; 5082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with Esp15 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab), sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant) agonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH2-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis).
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                                                                        LeuProProValLeuProProGluTyrIleProProSerPheArgArg
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                                                                                                                        ACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCA
                                                                                                                                                                                                          CCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTC
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CC The present invention specifically describes mammalian Esel and 2
CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain
CC regulator of endocytosis). (I) are involved in regulation of clathrin-
CC mediated endocytosis (as a complex with Espl5 protein), vesicular
CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists,
CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab);
CC sequences antisense to the (I) polynucleotide; agents that downregulate
CC to treat diseases associated with undesirable endocytosis and resulting
CC changes in cellular function. Particularly overexpression of Esel is used
CC to block clathrin-mediated endocytosis in vivo or in cell cultures, while
CC (Ant)agonists of (I) is used to promote endocytosis of selected cells.
CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of
CC cells that can be stimulated to proliferate by a growth factor receptor;
CC and similar compounds (also inactive Ese mutants) can be used to prevent
CC viral infection. Endocytosis may also be regulated, in vivo or in cell
CC cultures, by forming an Ese-Espl5 complex, then binding dynamin to the
CC complex. Generally conditions that can be treated include cancer;
CC abnormal cell division or migration; viral infection; or abnormal
CC receptor signalling, tissue development or synaptic transmission. The
CC present sequence represents mouse Esel.
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                                                                                          Percent Similarity:
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05-FEB-1999;
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                                                                                                                                                                                  Sequence 5144 BP; 1447 A; 1298
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                                                                                                                                No
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                                                                                                                                                                                                                      represents mouse
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   x AAZ39025
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Indels:
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 (1-5144)
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ID AAZ3
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                         region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorder, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations
                                                                                                                                                                                                                                                                          This is the nucleotide sequence of full-length cDNA (clone 11) contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the small candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 10;
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   including brain malformations microcephaly, lissencephaly,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH3DIA gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryoctyic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a nucleic acid that expresses SH3DIA or its antisense
                                                 AAZ34571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains chromosome 21 with leukaemias, neural abnormalities, dysfunctions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3D1A gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of full-length cDNA corresponding to novel human SH3 gene, termed the SH3D1A gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5199 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys
                                                                                                                                                                                                                       ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro
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                                                                                                                                                      LeuProProValLeuProProGluTyrIleProProSerPheArgArg
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                                                                                                                                                                                            ACAGCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA
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1 TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys

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US-09-720-934-2_COPY_215_310 (1-96)
                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                        CC This is the nucleotide sequence of full-length cDNA (clone 21)
CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that
CC contributes to the development of platelets and the pathogenesis of
CC leukaemias, both in general and in particular those involving the
CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate
CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate
CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at
CC least 3 isoforms exist. The invention provides methods for the diagnosis
CC and treatment of megakaryocytic abnormality, myeloproliferative disorder,
CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia,
CC platelet disorder on chromosome 21 with leukaemias, neural
CC association of gains in chromosome 21 with leukaemias, neural
CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly,
CC and colpocephaly. Methods are also provided for: suppressing cells unable
CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly,
CC and colpocephaly. Methods are also provided for: suppressing cells unable
CC to regulate themselves; screening for a somatic alteration in the SH3D1A
CC gene, monitoring the progress or megakaryocytic abnormality, myeloproliferative
CC disorder, haematopoietic disorder, platelet disorder or leukaemia; and
CC treatment of a subject (including a prenatal subject) having
CC merakerocytic abnormality, myeloproliferative
                                                                                                                                                                                     Sequence 5458 BP;
                                                                                                                                                                                                                        megakaryocytic abnormality, myeloproliferative disorder, disorder, leukaemia or neural disorder using a nucleic acexpresses SH3D1A or its antisense nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 8; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korenberg JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoietic disorder; cognitive dysfunction; microcephaly; ss. lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3D1A gene; human;
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The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-cCC mediated endocytosis (as a complex with Esp15 protein), vesicular CC mimetics, fragments and inactive mutants); (I) (or its (ant)agonists, CC sequences antisense to the (I) polynucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are used CC to treat diseases associated with undesirable endocytosis and resulting CC changes in cellular function. Harticularly overexpression of Esel is used CC administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or ab are used to suppress abnormal proliferation of CC cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding Esel and 2 endocytosis, used e.g. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5738 BP;
                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID
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                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                       nervous
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                                                                                                                                                                                                                                                                                                                                                                                     AAI80000
                                                                                                                                                                                                                                                                                                                                                                                                               AAI80000 standard; cDNA; 548
                                                                                                      (HYSE-)
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                                       2001-514838/56.
DB; AAO00069.
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                                                                                                     HYSEQ INC
                                                                                                                                                                                                                                                                      system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuProProValLeuProProGluTyrIleProProSerPheArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCAGGCTCAGCTTGAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTC
                                                                             Liu
                                                                                                                              2000US-00515126.
2000US-00577409.
                                                                                                                                                                   2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                           Ç
                                                                                                                                                                                                                                                                       disorders; arthritis;
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                          inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dynamin to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021
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Isolated nucleic acids and polypeptides, useful for and treating e.g. leukemia, inflammation and immune

preventing disorders.

diagnosing

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Best Local
Query Match
DB:
      RESULT 13
ABK43498
ID ABK43
XX ABK43
XX ABK43
XX OS-JU
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-JU
CT 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-720-934-2_COPY_215_310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                    hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder, Albeimer's disease; AlbS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes, cancer; leukaemia; neovascularisation; endocrine disorder; renal disorder; kidney failure; blood disorder; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibit activity and may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity had may be useful in the diagnosis and/or restment for activity had may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity and may be useful in the diagnosis and/or restment for activity and restment for activity and may be useful in the diagnosis and/or restment for activity and setting the diagnosis and/or restment for activity and setting the diagnosis and/or restment for activity and setting the diagnosis and/or restment for activity activity and setting the diagnosis and/or restment for activity activity and setting the diagnosis and/or restment for activity activity and setting the diagnosis and or restment for activity activity and setting the diagnosis and or restment for activity activity and setting the diagnosis and or restment for activity activity and setting the diagnosis and or restment for activity activity activity activity activity activity and setting the diagnosis activity activity activity activity activity and setting the diagnosis activity act
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         WO200155318-A2
                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK43498
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                                                                                                                        additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuProProValLeuProProGluTyrIleProProSerPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 60; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCACCTGTCCTGCCTCCAGAATACATTCCACCTTCTTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACAGGCTCAGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                         novel central nervous system protein #78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                        tood
                                                                                                                                                                                                                                                                                                                                                                                   system; CNS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173
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496.00
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                                                                                                                        preservative;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                     gene therapy; gene; ss.
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14-JUL-2000

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14-JUG-2000

16-JUG-2000

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30-JUN-2000;
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24-FEB-2000;
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17-MAR-2000;
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2000US-022964P.
2000US-0224519P.
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2000US-0231243P.
2000US-0233063P.
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2000US-02342399P.
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2000US-0214886P.
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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                Rosen CA,
                                                (HUMA-) HUMAN GENOME
                Barash SC,
                                                                                                                                                2000US-0241785P

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                                                 SCI INC.
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Alignment Scores:

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DR P-PSDB; AAU87168.

XX New isolated nucleic acid encoding a protein for diagnosing, preventing, proteining or ameliorating medical conditions and used as food additives or treating or ameliorating medical conditions and used as food additives or processoratives.

XX Claim 1; SEQ ID NO 88; 837pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a convel central nervous system protein. (I) and polypeptides (III) encoded CC by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include convel central nervous system protein are diagnosed or treated include by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include convel central sclerosis, infections are diagnosed or treated include convel central sclerosis, infections caused by bacteria, viruses c.g. cardiac arrest, cerebrovascular disorders e.g. Alzhaimer's disease and convel trophic lateral sclerosis, infections caused by bacteria, viruses c.g. anglogenesis, nervous system disorders e.g. Alzhaimer's disease and convel trophic lateral sclerosis, infections caused by bacteria, viruses c.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cc e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cc e.g. corneal infection, gastrointestinal disorders e.g. diabetes can disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes can pituitary dwarfism, cancers and disorders at the cellular level e.g. cc espiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. calcute kidney failure and blood related disorders e.g. myocardial contents before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The content protein, to increase or decrease storage capabilities, fat content, lipid, protein,
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RESULT 14 AAI63825 Percent Similarity:
Best Local Similarity:
Query Match:
DB: X B X B X B X B X 밁 Ó 밁 S 밁 S 뭐 8 뮍 Š US-09-720-934-2_COPY_215_310 (1-96) Score Human polynucleotide SEQ ID NO 33 AAI63825 No.: 22-OCT-2001 AAI63825; 1041 981 921 198 801 TGGGCTGTTCCTCAGTCATCAAGACTGAAATACAGGCAATTATTCAATAGTCATGACAAA 57 37 77 21 ThrMetSerGlyHisLeuThr------۳, CAGTCAAGTTTACCACAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAA TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys GATGGAAAACTTACAGCAGAAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATG GlnSerSerLeuProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGln SerGlyGlnProLeuProProValLeuProProGluTyrIleProProSerPheArgArg AspGlyLysLeuThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMet standard; cDNA; 3466 TCTGGCCAACCACTGCCACCTGTCCTGCCTCCAGAATACATTCCACCTTCTTTAGAAGA 1100 (first entry) 8.17e-51 489.00 96.00% 96.00% 97.60% x ABK43498 (1-3319) Length: Matches: Gaps: Mismatches: Indels: Conservative: -GlyProGlnAlaArgThrIleLeuMet 96 76 56 36 860 20 980 920 1040

MAR-2000; 2000US-0190076 MAY-2000; 2000US-019813 MAY-2000; 2000US-019813 MAY-2000; 2000US-019813 MAY-2000; 2000US-0214886 MUN-2000; 2000US-0214886 MUN-2000; 2000US-0216880 MUN-2000; 2000US-0216880 MUN-2000; 2000US-0216880 MUN-2000; 2000US-0217486 MUN-2000; 2000US-0217486 MUN-2000; 2000US-0217486 MUN-2000; 2000US-022954 MUN-2000; 2000US-0225214 MUN-2000; 2000US-022526 MUN-2000; 2000US-0225276 MUN-2000; 2000US-0231441 MUN-20000US-0231440 MUN-20000S-0231440 MUN-20000S-0231440 MUN-20000S-0231440 MUN-2000S-0231440 MUN-2000S-0231440 MUN-2000S-0231440 MUN-2000S-0231440 MUN-2000S-0231440 MUN-2000S-0231440 MUN-2000S-023144	04-FEB-2000; 20000 24-FEB-2000; 20000 02-MAR-2000; 20000 16-MAR-2000; 20000	17-JAN-2001; 2001WO-US00130 31-JAN-2000; 2000US-0179065	02-AUG-2001.	AA PN WO200155308-A2. XX	AA OS Homo sapiens.	antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss.	<pre>neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; anti</pre>	Human; antiarthritic; a cerebroprotective; noot fungicide; ophthalmolog
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, hutoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disprders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acids and polypeptides, useful for diagnosing treating and/or preventing human diseases and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3466 BP; 1056 A; 829
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LysThr--MetSerGlyHis-LeuThr-GlyProGlnAlaArgThrIleLeuMetGlnSe 38 TGGGCTGTTCCTCAGTCAAAGACTGAAAAATACAGGCAAATTATTCAATAGTCATGAC

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Alignment
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                                                                                                                                                                                                                                                                                      CC genes. (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a college of the sequences, as molecular weight markers and as a food college of sites expressing (II). (I) and (II) are useful in medical imaging converting and polynucleotide sequences have applications in college of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The college of sites expression, and the sequences have applications in college of darances, forensics, gene mapping, identification of mutations college of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and canding sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this collection of the printed specification, but was obtained in collection in format directly from WIPO at the collection of the printed specification, but was obtained in collections and intentions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences. (I) is useful as hybridisation proces, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mappi and in recombinant production of (II). The polynucleotides are also in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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food supplement; medical imaging; diagnostic; genetic disorder; ss
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58	38 rSerLeuProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGl 58		δ
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-USER=US09720934_@CGN 1 1 284_@runat_30062004_064540_13455 -NCPU=6 -ICPU=3
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-09-338-933-72
US-09-215-681-72
US-09-216-003A-72
US-09-215-681-60
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US-09-404-879A-72
                                  US-09-720-934-2_COPY_215_310 (1-96) x US-09-404-879A-72 (1-2017)
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
EITE DEFENICE. JOINTA 4600
                                                                                                                                                                                                                                                  LENGTH: 2017
TYPE: DNA
ORGANISM: Homo:
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CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20
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Matches:
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21 ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40 TGGGCAGTTCCTCAGCCTTCAAGATTAAAGTATCGGCAAAAATTTAATAGTCTAGACAAA

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo Sapien
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Sequence 72, Application US/0921
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
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US-09-216-003A-72
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; ORGANISM: Homo sapien
US-09-215-681-72
US-09-720-934-2_COPY_215_310 (1-96)
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LENGTH: 2017
TYPE: DNA
ORGANISM: Homo
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SEQ ID NO 72
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.462
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CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: PatentIn Ver. 2.0
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RESULT 6
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; ORGANISM: Homo
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US-09-404-879A-60
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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LENGTH: 480
TYPE: DNA
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
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APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REPERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 310 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/215,681A CURRENT FILING DATE: 1998-12-17
                                                                                                       ORGANISM: Homo
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
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GENERAL INFORMATION:
                                     SEQ ID NO 5
LENGTH: 531
                                                                                                                                                                                                                                                                               Sequence 5, Application US/09338933 Patent No. 6488931
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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TYPE: DNA
ORGANISM: Homo
                                                                                                     NUMBER OF SEQ ID NOS: 312
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA ORGANISM: Homo sapien
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Indels:
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Sequence 5, Application US/09215681A
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT FILING DAYE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 531
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SEQ ID NO 5
LENGTH: 531
TYPE: DNA
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APPLICANT: Mitcham
APPLICANT: Frudaki
                                                                                                                                                                          Sequence 3, Application Patent No. 5487979 GENERAL INFORMATION:
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                                                                       APPLICANT: DiFiore, F
APPLICANT: Fazioli, F
TITLE OF INVENTION: F
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
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            CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
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                                                                                          Francesca
A Substrate for the Epidermal Growth
Factor Receptor Kinase
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Query Match:
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                                                                                                Sequence 3, Application Patent No. 5717067
                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
               APPLICANT: Diffiore,
APPLICANT: Fazioli,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NJH060.001A
TELECOMMUNICATION INFORMATION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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LOCATION:
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   Prancesca A Substrate for the Epidermal Growth Factor Receptor Kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/480
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095
FILING DATE: 22-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSCH, Ned A
REGISTRATION NUMBER: 09/65
REFERENCE/DOCKET NUMBER: NIHC
TELECOMMUNICATION INFORMATION:
TELECHNUM: (619) 235-8550
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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                                                 711 GTGCCAATGTCCTTGCCTCCAGCCTTGGTGCCACCTTCTAAGAGAAAA 758
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                                                                               LeuProProValLeuProProGluTyrIleProProSerPheArgArg
                                                                                                                   CCTGTGGAAATCCTTGGAAGAGTTTGGGAGTTGAGTGATATTGACCACGATGGAAAGCTG
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SYSTEM: PC-DOS/MS-DOS
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Matches:
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Sixteenth Floor
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Sequence 3, Application US/08477389

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Best Local Similarity:
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GENERAL INFORMATION:
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FILING DATE: 07-UTN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/095,737
FILING DATE: 22-UTL-1993
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPROV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Difiore, Pier P
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
TITLE OF INVENTION: Factor Receptor Kinase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: California
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LENGTH: 3033 base pairs
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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591
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Gaps:
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Matches:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09720934 @CGN 1 1 1500 @runat 30062004 064541 13481
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XOAPDP=10 -XGAPEXT=0.5
-FGAPPOP=6 -FGAPEXT=7 -YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                       /cgn2_6/ptodata/1/pubpna/US09A_UBCOMB.seq:*
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Result

Score

Query Match Length

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Description

Percent Similarity: Alignment Scores: Pred. No.: US-09-764-875-88

8.22e-60 489.00 96.00%

Conservative: Length: SOFTWARE: PatentIn Ver. SEQ ID NO 88

LENGTH: 3319
TYPE: DNA
ORGANISM: Homo sapiens

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1249

score

RESULT US-09- ; Sequ ; Publ ; GENE ; APP ; TIT ; FIL ; CUR ; CUR			۸. ۸		4	4.	.K. 1	با بد	1 [4]	(O La		1					K 2		מ	N)	N) 1		٠.	ц	ы 6	ب د		_	L L	. ب								-
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Protei:
FILB REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
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Publication No. US20040014039A1
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US-09-884-441-72
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                                                                                                                                            Sequence 72, Application US/09907969 Publication No. US20030091580A1 GENERAL INFORMATION:
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APPLICANT: Cartear, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
                                                                                                            APPLICANT: Mitcham, Jennifer L. APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2017
TYPE: DNA
ORGANISM: Homo
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CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
                                                     APPLICANT:
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                                Algate, Paul A.
Fling, Steven P.
Retter, Marc W.
Fanger, Gary Richard
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Reed, Steven G.
Vedvick, Thomas S.
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APPLICANT: Hill, Paul
APPLICANT: Albone, Earl
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46208
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 2017
 Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-09-827-271-72
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US-09-907-969-72
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LENGTH: 2017
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APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary F
                                                                                                                                                                                                                                                                                                                  Sequence 72, Application US/09827271 Publication No. US20030165504A1
                                                                                                                                                                                                      APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.46206

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSEQ for Windows Version
                                                                                                                          ORGANISM: Homo
                                                                                                                                        TYPE: DNA
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Hill, Paul
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US-10-198-053-72
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo
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US-09-720-934-2_COPY_215_310 (1-96)
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Publication No. US20030124140A1
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APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
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81 LeuProProValLeuProProGluTyrIleProProSerPheArg
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Best Local Similarity:
                                                                                         US-09-764-881-54
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Sequence 54, Application US/097648B1
Publication No. US20030125248A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/103988B5A Publication No. US20040053282A1
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APPLICANT: Obayashi, Masaya
APPLICANT: Saito, Hirohisa
APPLICANT: Takahasi, Biki
TITLE OF INVENTION: Method of Tesbing For Allergic Diseases
FILE REFERENCE: SHIMIZU-07907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2000-314093 PRIOR FILING DATE: 2000-10-13
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/JPO1/08937
PRIOR FILING DATE: 2001-10-11
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APPLICANT: Hashida, Ryo
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LOCATION: (7)..(50
OTHER INFORMATION:
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OTHER INFORMATION: Synthetic
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TYPE: DNA
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Ogawa, Kaoru
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Matches:
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US-09-764-875-91

Sequence 91, Application US/09764875

Publication No. US20040018969A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: DJ002

CURRENT FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/09/764,875

CURRENT FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 1249

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 91
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Best Local Similarity:
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
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NAME/KEY: SITE
LOCATION: (550)
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OTHER INFORMATION:
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NAME/KEY: SITE
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LOCATION: (934)
LENGTH: 955
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LOCATION: (944)
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                                                                                                                                                                                                                                                    Sequence 54, Application No. US20 GENERAL INFORMATION:
                                                                                                                               SOFTWARE: P
SEQ ID NO 54
                                                                                                                                          Prior application data removed - refer to NUMBER OF SEQ ID NOS: 192 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (934)
                                           ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (550)
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OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
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No. US20020086821A1
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                                                                                              PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 54, Application No. US20 GENERAL INFORMATION
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/764,881
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
                   PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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Prior Application
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Sequence 34, Application US/10158057
Publication No. US20040014039A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ05C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
CURRENT FILING DATE: 2002-06-12
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US-10-158-057-34
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Best Local Similarity:
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                Prior Application removed - See
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 955
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: ELANTS WITH IMPROVED PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
UNMBER OF SEQ ID NOS: 47374
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US-10-369-493-36727
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; TYPE: DNA
; ORGANISM: Aspergillus
US-10-369-493-36727
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APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/09884441 Patent No. US20020119158A1
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                               ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
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LENGTH: 480
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mitcham, Jennifer L. APPLICANT: King, Gordon E. APPLICANT: Algate, Paul A.
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2001-07-17
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                                                                        233 GACCAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTGCAGGGCCAACAG
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Hill, Paul
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Vedvick, Thomas S.
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Fanger, Gary Richard
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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   27513289 seqs, 14931090276 residues
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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	_	R96004 A	6839 MR2-	m	AW668653 111193 MA	BG107389 602290786	5187	9325	4367	9	/ AGEN		AALS4049 mgsacos	240	, ,	AGENCOUR	, ,	uraugua.	ALSSISBS	Z TOBAPI	OT-M-GHO		, (E50150	1220693	F039131	406T8GE	١	1/5/	G161771 de42d08.	· W	65 BX75876	0 6031425	AL870708) RC1-	Mus	BC020269 Homo sapi	3 Homo	BQ719508 AGENCOURT	N	CA750495 UI-M-FY0-	CF742748 UI-M-HB0-	308 UI-M-	BM728997 UI-E-EO1-	CF532126 UI-M-GH0-	Description

ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	CF532126	RESULT 1
Mammaila; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 625)	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus (house mouse)	EST.	CF532126.1 GI:34584094	CF532126	IMAGE:30356524 5', mRNA sequence.	UI-M-GH0-cgu-d-05-0-UI.rl NIH_BMAP_GH0 Mus musculus cDNA clone	CF532126 625 bp mRNA linear EST 12-SEP-2003		

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TITLE
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: pYX-5
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                                                  LeuProProValLeuProProG|uTyrIleProProSerPheArgArg 96
                                                                                                                                                                                                  ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro 80
                                                                                                                                                                                                                                                                                                                                                                      ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60
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                                                                                                                                                                                                                                                                                                    CCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type=""whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP GH0"
/clone lib="NIH BWAP Gh0"
/clone lib="NIH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developing Mouse Nervous System', supported by National Institute of Mehtal Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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AUTHORS
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                                                                                                                                      Query Match:
                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                         No..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UI-E-E01-aiw-e-23-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone UI-E-E01-aiw-e-23-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20
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319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="U1-E-E01"
/clone_lib="U1-E-E01"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-E01 is a normalized CDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA
                                                                                                                                                                                                                                                                                                                                                    synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT713.-Pac vector. The oligomuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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1 to 641)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEBRF, Iowa City, IA 52242,
                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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JOURNAL COMMENT
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Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 729)
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                                                                                   /tissue_type="whole brain"
/dev stage="wembryo 12.5dpc"
/lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FOO"
/clone_lib="NIH BMAP_FOO"
/clone_lib="NIH BMAP_FOO"
/clone_Torgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Procurement: Dr. Jim Lin,
                                            Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefi.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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UI-M-HB0-clm-c-18-0-UI.rl NIH_BMAP_HB0 Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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               /tissue_type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clome_lib="NIH BMAP_HB0"
/note="Organ: Eye; Vector: pYX- Asc; Site 1: EcoR I;
Site_2: Not I; The library was constructed according
                                                                                                                                                                    /organism="Mus mus
/mol_type="mRNA"
/strain="C57BL/6"
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RESULT 5
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                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                Mammalla; Eutheria; Rodehtia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CA750495.1 GI:25575732
EST.
Mus musculus (house mouse)
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The following repetitive elements were found in this cDNA sequence: 637-722, >(CAG)n#Simple_repeat Seq primer: pYX-5.
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                                                                                               This clone was contributed by the Brain Molecular Anatomy Project
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CF538122 736 bp mRNA linear EST 12-SEP-: UI-M-GIO-cho-b-09-0-UI.rl NIH_BWAP_GIO Mus musculus cDNA clone IMAGE:30536000 5', mRNA sequence. CF538122.1 GI:34590104 EST. Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M I (bases 1 to 736) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Introct SergiyH steuthrGlyProGlnAlaArgTnrIteLoumetGlnSerSerle	1.05e-46 Length: 732 501.00 Matches: 96 rity: 100.00\$ Conservative: 0 1100.00\$ Mismatches: 0 14 Gaps: 0 2_COPY_215_310 (1-96) x CA750495 (1-732) TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLysTyrAlgGlnLeuPheAsnSerHisAspLysTgGGCTCGTCAGTCAAAGGCTGAAATACAAGGCAGTTATTCAACAGCCACGACAAA	

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This clone was contributed by the Brain Molecular Anatomy Pro
BQ719508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                         /dev stage="membryo 13 5,14 5,16.5,17.5dpc"
//lab_host="DH10B (T1 phage resistant)"
//clone lib="MIH BMAP GIO"
//note="morgan: Brain; "vector: pyx- Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with BcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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US-09-720-934-2_COPY_215_310 (1-96) x BQ719508 (1-979)
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM13583 row: c column: 24
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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<u>ÁCAGCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA</u>
                                    ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro 80
                                                                                                                                                    ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60
                                                                                                                                                                                                                                                                             ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
                                                                                                                                                                                                                                                                                                                                                                              TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 20
                                                                                                          CCACAGGCTCAGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTT
                                                                                                                                                                                                                                                                                                                                             TGGGCTGTTCCTCAGTCATCAAGACTGAAATACAGGCAATTATTCAATAGTCATGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylc College of Medicine); available through Life Technologies."
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SaII; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                          1 TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLcuPheAsnSerHisAspLys
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http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: C Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4504796
This clone has the following problem: retained intron.
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Gene Collection (MGC), Chnoc
Institute, 31 Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia; Eutheria; Primþtes; Catarrhini; Hominidae; Homo.
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MAGE:3878242, mRNA.
ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu 60
                                                                  ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40
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                                                                                                                                                                                                                                                                                                                                                                              tissue_type="Ling, large/clone_lib="NIH_MGC_68"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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Homo sapiens, clone IMAGE:4899011,
EC020269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywiski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Con
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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1 (bases 1 to 2126)
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Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .nfo@bcgsc.bc.ca
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/clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:4899011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
4.79e-46
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Matches:
                                                                 Mismatches:
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                             epithelioid carcinoma"
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BC062938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-720-934-2_COPY_215_310 (1-96) x BC020269 (1-2126)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
Thomas L. Casavant.
                                                                                                                                                                                                                                                   Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC062938
BC062938.1 GI:38566052
HTC.
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                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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Query Match:
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                                                                       JOURNAL
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                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1, to 490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davi Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaef Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J. Casavant, T., Soares, M.B.
                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                    HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Pr
                                                                                                                                                                                                                                                                  RC1-BT0255-041099-011-c09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortiun Series: Plate: Row: Column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: bento-soares@uiowa.edu;
                                                                      Unpublished (1999)
                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                 AW370310.1
                                                                                                                                                                                                                                                                                    AW370310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://genome.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCAGGCTCAGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                LeuProProValLeuProProGluTyrIleProProSerPheArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _COPY_215_310 (1-96)
 Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone has the following problem: frame shifted
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Brain"
/clone_lib="NIH_BMAP_
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pYX-ASC"
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                                                        sequence.
AL870708
AL870708.2 GI:38665439
AL870708.2 GI:38665439
EST.
Silurana tropicalis (western clawed frog)
Silurana tropicalis
Silurana tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
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AL870708
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project: This entry can be seen in the following URL
(http://www.ludwig.org.bf/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0255-
041099-011-c09&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence start: 24
High quality sequence start: 489.
                      1 (bases 1 to 842)
Croning, M.D.R., Ashurst,
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Fax: +55-11-2707001
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g,M.D.R., Ashurst,J.
Xenopus tropicalis
                                                                                                                                                                                                                                        XGC-egg
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    .L., Taylor,R., Zorn,A.M. a EST project 2001 (11_2003)
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CDNA was oligo dT primed from 5ug of poly A+ RNA
ECORI-NotI cut cDNA was then ligated into pCS107
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site_2: NotI
Host: Escherichia coli_x11-blue.
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On Sep 15, 2002 this
Contact: Taylor R
Sanger Institute
                                   Gallus gallus (chicken)
Gallus gallus
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Email: trop@sanger.ac.uk
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                         EST
                                                                                                             sequence.
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/dev stage="Fegg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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 BX758765
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/mol_type="mRNA"
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="Female"
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db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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US-09-720-934-2_COPY_215_310 (1-96)
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81 LeuProProValLeuProProGluTyrIleProProSerPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) :
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from :
gastrulae. EcoRI-NotI cut cDNA was then ligated into p0
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli KL1- blue.
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Croning,M.D.R., Ashurst,J.L.,
Sanger Xenopus tropicalis EST
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                  1 TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Croning MDR Sanger Institute
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Amphibia; Batrachia; Anura; Mesobatrachi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Silurana.
                                                                     ThrAlaGluGluPheIleLeuAlaMetHisLeuIleAspValAlaMetSerGlyGlnPro
                                                                                                                                         CCGCAGAGCCAGCTAGCTACGATATGGAACCTTTCAGACATTGACCTAGATGGAAAACTA
                                                                                                                                                                    ProGlnAlaGlnLeuAlaSerIleTrpAsnLeuSerAspIleAspGlnAspGlyLysLeu
                                                                                                                                                                                                                                ACCATGAGTGGGCATTTAACAGGTCCTCAAGCAAGAACTATTCTTATGCAGTCAAGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone lib="XGC-gastrula" | ALL PLUE" |
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
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/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
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	ment Scores: .No.: 483.00 2: 483.00 2: 50.00 2: 1.46e-44 483.00 2: 1.0cal Similarity: 96.84% 1.0cal Similarity: 96.41% 1.0cal Similarity: 1.0cal	Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2/ TROPICALIS SEQUENCE ID: Ineualin07.qlkT Sequencing primer: T7 This sequence is from a Xenopus Gene Co. constructed by Aaron M. Zorn. cDNA, was oligo dT primed from 5ug of po. ECORI-NotI cut cDNA was then ligated in/ 5' end and NotI at the 3 end. Vector: pCS107; Site 1: EcoRI; Site_2: 1 Location/Qualifiers 1. 853 /organism="Silurana tropicalis/mol_type="mRNA"/db xref="taxon:8364" /db xref="taxon:8364" /dav_stage="neutula" /lab_host="Bschbrichia coli DH:/clone_11b="xGC-neurula" /note="Vector: pCS107; Site 1: was oligo dT primed from 5ug oligo dT prim	BX695683 XGC-neurula Silurana mRNA sequence. BX695683 XGC-neurula Silurana mRNA sequence. BX695683 I GI:38357890 EST. Silurana tropicalis (western Silurana tropicalis Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; M Xenopodinae; Silurana. 1 (bases I to 853) 1 (croning,M.D.R., Ashurst, J.L., Sanger Xenopus tropicalis EST Unpublished (2003) Contact: Croning MDR Sanger Institute Sanger Institute Hinxton, Cambridgeshire, CB10
ThrMetSerGlyHisLeuThrGlyProGlnAlaArgThrIleLeuMetGlnSerSerLeu 40	Pes: 1.46e-44 483.00 483.00 Matches: 92 rity: 98.95% Conservative: 2 13arity: 96.41% Mismatches: 1 10dels: 0 2 2 COPY_215_310 (1-96) x BX695683 (1-853) TrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPheAsnSerHisAspLys 13	EST project 2001 Inequilin07.q1kT7 Exenopus Gene Collection (XGC) library Zorn. Efrom Sug of poly A+ RNA from neurula. Then ligated into pCS107 with EcoRI at the EcoRI; Site_2: NotI H10B. iers rana tropicalis" "8354" 107" "108" rula" rula" pCS107; Site_1: EcoRI; Site_2: NotI; cDNA imed from Sug of poly A+ RNA from neurula. CDNA was then ligated into pCS107 with end and NotI at the 3' end."	853 bp mRNA linear EST 17-NOV-2003 (Silurana tropicalis cDNA clone TNeu111n07 3', 890 (western clawed frog) Chordata; Craniata; Vertebrata; Euteleostomi; Anuka; Mesobatrachia; Pipoidea; Pipidae; La. Craniata; Carn,A.M. and Rogers,J. Ccalis EST project 2001 (11_2003)

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Search completed: July 1, 2004, 19:48:34 Job time: 2895.87 secs

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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first 45 summaries
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              US-08-630-915A-193

US-09-833-381-1294

US-08-475-894-3

US-08-484-710-3

US-08-484-709-3

US-08-474-697-3

US-08-475-894-1

US-08-484-710-1

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US-08-671-354-1
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Sequence 1, Appli
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Sequence 1294, Ap
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ALIGNMENTS

US-08-630-915A-193

RESULT 1

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LIPE: Floppy disk

LOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PALICATION DATA:
APPLICATION MUMBER: US/A

CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR TO THE CLASSIFIATION OR THE CLASSIFIATION O
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
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KAY, Bria
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Best Local Similarity:
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                                                                                                                                                                                                                                       Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1294
LENGTH: 970
TYPE: DNA
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APPLICANT: Robison, Keith
TITLE OF INVENTION: No. 66
FILE REFERENCE: 5800-119
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 basss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo
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STRANDEDNESS: single
                                                316 ATTGTGATTATACACGAGAAAAAA-----GAAGAAGGATGGTGGTTTGGATCTTTGAAT
                                                                                                                  376 AAGGCCTTGTATTCTTTTCAAGCCAGGCAAGATGATGAGTTGAATTTGGAAAAGGGTGAC
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                                                                                                                                       4 ValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIleGln
GlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIlePro
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Mismatches:
Indels:
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Matches:
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US-08-475-894-3
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                                                                             Sequence 3, Application Patent No. 5656438
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               GENERAL INFORMATION:
APPLICANT: Yen-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . No.:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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LENGTH: 1392 base pair
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ADDRESSEE: LAHIVE & COCKFIELD
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
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REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE
                                                                                                                                                                                                                                                                            Sequence 3, Application US/08484709 Patent No. 5837844
GENERAL INFORMATION:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   TITLE OF INVENTION: THE CAIP-LII
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Louis Myers
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ZIP: 02109-1875
SOFTWARE:
                                                                                        COUNTRY: USA
ZIP: 02109-1875
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                                                                                                                                                                   60 State Street, Suite 510
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//ENTION: THE CAIP-LIKE GENE FAMILY
PatentIn Release #1.0,
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,69
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yen-Ming TITLE OF INVENTION:
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                                                                                             NAME:
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                                                                           NAME: Louis Myers REGISTRATION NUMBER:
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                                                                                                                                    FILING DATE:
CLASSIFICATION:
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; MOLECULE TYPE: CDNA US-08-475-894-1
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Best Local Similarity:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,894
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APPLICANT: Yen-Mi
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                                                                                                                                                                  TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                 NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: lin
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VENTION: THE CAIP-LIKE GENE FAMILY
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Best Local Similarity:
Query Match:
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Patent No. 5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Louis Myers
REGISTRATION NUMBER: 35,
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                              No.:
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                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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OPERATING SYSTEM:
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1027 TACTGCAAAGTAATATTTCCATATGAGGCACAGAATGATGATGAATTGACAATCAAAGAA 1086
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/ENTION: THE CAIP-LIKE GENE FAMILY
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SYSTEM: PC-DOS/MS-DOS
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RESULT 10
US-08-474-697-1
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Best Local Similarity:
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APPLICANT: Yen-Mi
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LENGTH: 1659 base pairs
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
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CLASSIFICATION:
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STRANDEDNESS: both
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                          Sequence 1, Application US/08671354
Patent No. 6423824
                                                         GENERAL INFORMATION:
APPLICANT: Hsu, Yen-Ming
TITLE OF INVENTION: THE (
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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ADDRESSEE: LAHIVE & COCKFIELD
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TITLE OF INVENTION: THE
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                                                                                               CAIP-LIKE GENE FAMILY
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Indels:
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Best Local Similarity:
                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                         US-08-306-691B-48
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                                                                    Sequence 48, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIJECTION NUMBER: US 00, APPLICATION NUMBER: US 08/484,709
APPLICATION NUMBER: US 08/484,709
APPLICATION NUMBER: US 08/475,894
APPLICATION NUMBER: US 08/475,710
TITING DATE: 07-JAN-1995
APPLICATION NUMBER: US 08/475,710
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TITLE OF INVENTION:
                                  APPLICANT:
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LENGTH: 3143 base pair
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ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JAN-1995
APPLICATION NUMBER: US 08/475,710
FILING DATE: 07-JAN-1995
APPLICATION NUMBER: US 08/474,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
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                                  Calabretta, Bruno
Skorski, Tomasz
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Matches:
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                                                                                                                                                                                                                                                                       RESULT 13
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Best Local Similarity:
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                                                                                                                                                     Sequence 79, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83:
TELECOMMUNICATION INFORMATION:
                                                                                                      NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS: SCULLY, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 1
FILING DATE: September
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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ADDRESSEE: Seidel, Gonda,
STREET: Two Penn Center,
COMPUTER READABLE FORM:
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                               COUNTRY:
                                                        STATE:
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TELEFAX: (215) 568-5549
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ber 15, 1994
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Suite 1800
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MEDIUM TYPE:

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Best Local Similarity:
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                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Vav Proto-Oncogene Protein NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                    ATTORNEY/AGENT INFORMATION:
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                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                          FILING DATE:
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                COUNTRY:
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Timothy J.
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                                                                                                                  Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08630915A
Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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              FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linea MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pair
TYPE: nucleic acid
                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,915A
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                            STATE: New York
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REGISTRATION NUMBER:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: July 1, 2004, 19:53:46
Job time: 47.7143 secs
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                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEY: 66141 PENNIE
INFORMATION FOR SEG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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                                                  326 GCAGAATCCATT 337
                                                                                                    266 TGGAAAGGGACATGCAAGGGCAGAACAGGACTGATCCCGAGCAACTATGTGGCTGAGCAG 325
                                                               57 AlaGluLysIle 60
                                                                                                                22 IleGlnProGlyAspIleValMetVal---AspGluSerGlnThrGlyGluProGlyTrp 40
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57.81%
43.75%
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Matches:
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Mismatches:
Indels:
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-O=(cgn2 1)(USPTO_spool p)(US09720934/runat 30062004_064541_13481/app_query.fasta_1.1386
-O=(cgn2 1)(USPTO_spool p)(US09720934/runat 30062004_064541_13481/app_query.fasta_1.1386
-DB=Published_Applications_NA -QFMT=fastap_ -SUFFIX=rnpb -MINMATCH=0.1
-COOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MXX=100
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-MAXLEN=2000000000 -USER-US09720934_@CGN 1 1 1500 @TUNAT 30062004_064541 13481
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-LONGIOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Query
Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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14 US-10-288-798-36
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6 US-10-158-057-33
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US-09-764-868-125
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Sequence 88, Appl Sequence 176, App Sequence 175, App Sequence 177, App Sequence 193, App Sequence 193, App Sequence 1934, App Sequence 1934, App Sequence 10314, App Sequence 10314, App Sequence 1655, App Sequence 1655, App Sequence 1724, App Sequence 1725, App Sequence 1726, App Sequence 1726, App Sequence 187, App Sequence 187, App Sequence 1870, App Sequence 1873, App Sequence 155, Appl Sequence 15441, Sequence 15441, Sequence 1714, Appl Sequence 1714, Appl Sequence 1714, Appl Sequence 1871, App
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ALIGNMENTS

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RESULT 1
US-09-764-875-88
; Sequence 88, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PJZ02
Percent Similarity:
                                      Alignment Scores: Pred. No.:
                                                                                            ; LENGTH: 3319
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-875-88
                                                                                                                                                                         SOFTWARE: Pa
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: Patentin Ver. 2.0
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  Matches:
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US-10-158-057-33
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                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/10158057
Publication No. US20040014039A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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NAME/KEY: misc feature
LOCATION: (3194)

TANFORMATION: n eq
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CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3466
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (3465)
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Pro 61
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                                                                                                                                                                                 GTAAAAGTGGTGTATTACCGGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAAATC
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US-09-720-934-2_COPY_740_800 (1-61) x US-09-764-868-125 (1-4210)
                                         Query Match:
DB:
                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                   Alignment Scores: Pred. No.:
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Best Local Similarity:
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SEQ ID NO 176
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                                                                                                                                                                                                             LENGTH: 4210
TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                          Prior application data removed NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
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TYPE: DNA
ORGANISM: Homo sapiens
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No.:
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US-09-720-934-2_COPY_740_800 (1-61) x US-10-398-885A-15 (1-5828)
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                                                                                US-09-879-957-193
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                 Sequence 193, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
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Publication No.
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TITLE OF INVENTION: Method of Testing For Allergic Diseases
FILE REFERENCE: SHIMIZU-07907
CURRENT APPLICATION NUMBER: US/10/398,885A
CURRENT FILING DATE: 2003-08-11
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APPLICANT: Hashida, Ryoichi
APPLICANT: Ogawa, Kaoru
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PRIOR APPLICATION NUMBER: PCT/JP01/08937
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: JP 2000-314093
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                2233 TTGGTGAATTATAGAGCATTATACCCCTTTGAAGCAAGGAACCATGATGAGATGAGTTTT 2292
APPLICANT: SPARKS, Andrew B.
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Saito, Hirohisa
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No. US20040053282A1
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Matches:
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Indels:
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Best Local Similarity:
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                   Sequence 17127, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
  APPLICANT: Penn, Sharron G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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APPLICATION NUMBER: US/09/879,957
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Cun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               291
                                                                                                                                                                                                                                                                                                                351 AGTTTTCAAGGÁAATTTTGGCTGGTTTCCATGCAATTATGTAGAAAAAATGCCA 404
                                                                                                                                                                                      44
                                                                                                                                                                                                                                                       24 ProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrpLeuGlyGly 43
                                                                                                                                                                                    GluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIlePro 61
                                                                                                                                                                                                                               TCTGGAGATATAATTCAGGTTGATGAAAAAACCGTAGGAGAACCTGGTTGGCTTTATGGT
                                                                                                                                                                                                                                                                                                                                                 ValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
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INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOFFMAN, No.
KAY, Brian K
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FOWLKES, Dana M.
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Matches:
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Indels:
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23

FEATURE FEATURE:

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RESULT 6

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Query Match:
                    Percent Similarity:
Best Local Similari
                                                                                                             Alignment Scores:
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SEQ ID NO 17127
LENGTH: 270
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OTHER INFORMATION: 1
OTHER INFORMATION: 1
OTHER INFORMATION: 1
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OTHER INFORMATION:
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OTHER INFORMATION:
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ORGANISM: Homo
FEATURE:
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PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-02-04
PRIOR REPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                            No.:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00668
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APPLICATION NUMBER: US 09/774,203
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                       Similarity:
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                                                                                                                                                                    ON: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

ON: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

ON: EXPRESSED IN LUNG, SIGNAL = 1.6

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

ON: EXPRESSED IN HEART, SIGNAL = 2.2

ON: EXPRESSED IN HEART, SIGNAL = 2.2

ON: EXPRESSED IN AD71263.1, EVALUE 1.00e-112

ON: SWISSPROT HIT: Q15811, EVALUE 2.00e-45

NI: NT HIT: g1115$6214, EVALUE 0.00e-45
                                                                                                                                                                                                                                                               N: MAP TO APO00193.1

N: EXPRESSED IN HELA, SIG

N: EXPRESSED IN HELA, SIG

N: EXPRESSED IN PLACENTA,

N: EXPRESSED IN 97474, SIG

N: EXPRESSED IN FATAL LIV

N: EXPRESSED IN LUNG, SIG

N: EXPRESSED IN DOLLT LIV

N: EXPRESSED IN DULT LIV
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                                                                                                                                                                                                                                                                                                                                                       PLACENTA, SIGNAL
BT474, SIGNAL =
                                                                                                                                                                                                                                                                                                                                                                                                 HBL100, SIGNAL = 2.2
HELA, SIGNAL = 1.6
BRAIN, SIGNAL = 2.3
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                                                                Length:
Matches:
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Mismatches:
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RESULT 8
US-09-864-761-26948
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PRIOR ETLING DATE: 2
PRIOR APPLICATION NU
PRIOR FILING DATE: 2
PRIOR APPLICATION NU
PRIOR FILING DATE: 2
PRIOR FILING DATE: 2
                                                                                                                                                                                          SEQ ID NO 26948
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Patent No.
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PRIOR EILING DATE: 2001-01-30
PRIOR PRIOR EILING DATE: 2001-01-30
PRIOR ADDITOR---
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SOFTWARE: Annomax Sequence
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                             TYPE: DNA
ORGANISM: Homo :
FEATURE:
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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OTHER INFORMATION: MAP TO APO00311.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL =
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SI
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL
                                                                                                                                                             ENGTH:
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OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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5. US20020048763A1
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 70/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron
APPLICANT: Rank, David F
APPLICANT: Hanzel, David
APPLICANT: Chen, Wensher
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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R INFORMATION:
FILING DATE: 2001-03
APPLICATION NUMBER:
FILING DATE: 2001-03
                                                                APPLICATION NUMBER: PCT/US01/00661
                                                                                          FILING DATE:
                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                      FILING DATE: 2001-01-30
                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
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Chen, Wensheng
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NN: EXPRESSED IN LUNG, SIGNAL = 0.66

NN: EXPRESSED IN BRAIN, SIGNAL = 0.69

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.1

NN: EXPRESSED IN HELA, SIGNAL = 0.9

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

NN: MIT HIT: AF114488.1, EVALUE 0.00e+00

NN: SWISSPROT HIT: Q15811, EVALUE 2.00e-45

NN: EST_HUMAN HIT: AA773263.1, EVALUE 1.00e-112
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US-09-864-761-30453
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Best Local Similarity:
                CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT ETLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
IITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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TYPE: DNA
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FILER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.7

FILER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

FILER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

FILER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.76

FILER INFORMATION: EXPRESSED IN HELIOO, SIGNAL = 1.3

FILER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

FILER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

FILER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 0.95

FILER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 0.95

FILER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 0.95

FILER INFORMATION: EXT HUMAN HIT: AA773263.1, EVALUE 1.00e-112

FILER INFORMATION: SWISSPROT HIT: Q15811, EVALUE 2.00e-45
APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                              Sequence 13884, Application Patent No. US20020048763A1 GENERAL INFORMATION:
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SEQ ID NO 311
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC JULIE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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ORGANISM: Homo
FEATURE:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/USQ1/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/USQ1/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USQ1/00668
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FILING DATE: 2001-01-29
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EXPRESSED IN HBL100,
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US/09/864,761
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DIN HBLA, SIGNAL = 1.6
DD IN BRAIN, SIGNAL = 2.3
DD IN PLACENTA, SIGNAL = 1.6
DD IN BT474, SIGNAL = 2
DD IN BT474, SIGNAL = 2
DD IN BONE MARROW, SIGNAL = 1.8
DD IN FETAL LIVER, SIGNAL = 3.2
DD IN LUNG, SIGNAL = 3.2
DD IN ADULT LIVER, SIGNAL = 2.7
DD IN ADULT LIVER, SIGNAL = 2.7
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US-09-720-934-2_COPY_740_800 (1-61) x US-09-864-761-13884 (1-475)
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Best Local Similarity:
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN HELLIOU, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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ORGANISM: Homo
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RAPLICATION NUMBER: PCT/US01/00669

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00665

OR FILING DATE: 2001-01-30

OR APPLICATION UMBER: PCT/US01/00668

OR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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GlyTrpPheProAlaAsnTyrAlaGluLysIlePro
                                                                                     ValAspGluSerGlnThrGlyGluProGlyTrpLeuGlyGlyGluLeuLysGlyLysThr 49
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US-09-864-761-10314
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US-09-864-761-10314
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OTHER INFORMATION: EXPRESSED IN ENT474,
OTHER INFORMATION: EXPRESSED IN HBL100,
OTHER INFORMATION: EXPRESSED IN HBL100,
OTHER INFORMATION: EXPRESSED IN FETAL I
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN PLACENT
OTHER INFORMATION: EXPRESSED IN PLACENT
OTHER INFORMATION: EXPRESSED IN HBLA,
OTHER INFORMATION: EXPRESSED INFORMATION: EXPRES
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
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NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00667
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ID IN BONE MARROW, SIGNAL = 1.1
ID IN HBL100, SIGNAL = 1.3
ID IN FETAL LIVER, SIGNAL = 32
ID IN LUNG, SIGNAL = 0.66
ID IN LUNG, SIGNAL = 0.69
IN BRAIN, SIGNAL = 0.69
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   Matches:
Conservative:
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SIGNAL = 0.92
LIVER, SIGNAL = (
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-833-381-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1294
LENGTH: 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
                                                                                                                                                                                                                                Sequence 1655, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1294, Application US/09833381
Patent No. US20020132090A1
                                   SOFTWARE: PatentIn
SEQ ID NO 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
                                                                                            CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
                                                         NUMBER OF SEQ ID NOS: 4096 SOFTWARE: PatentIn Ver. 2.
                                                                                                                                                                             TITLE OF INVENTION: No. : FILE REFERENCE: H1-A0105
                                                                                                                                                                                                                  APPLICANT: HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
TYPE: DNA
                  LENGTH: 2539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GTGGATGAAAGCCAAACTGGAGAACCCGGCTGGCTTGGAGGAGAATTAAAAGGAAAGACA
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                                                                                                                                                                                                                                                                                                                                                                                    GlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIlePro 61
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Indels:
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RESULT 15

US-09-918-995-14907

Sequence 14907, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

APPLICANT: HYSEQ, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENTIONE OF INVENTION: FROM VARIOUS CDNA LIBRAY

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/285,076

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Query Match:
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GlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIlePro 61
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Search completed: July 1, 2004, 20:15:55 Job time: 193.143 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum
Maximum
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-Q=/cgn2_1/USPTO_spool_p/US09720934/runat_30062004_064540_13442/app_query.fasta_1.1386
-Q=/cgn2_1/USPTO_spool_p/US09720934/runat_30062004_064540_13442/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09720934 @CGN 1 1.12421 @runat 30062004 064540 13442 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGC_SCORES=0 -WAIT -DSPBLOCKE100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=90 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match
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seq length: 2000000000
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Fgapop 6.0,
Delop 6.0,
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333
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	5	RESULT 1	
Hom	Hom	EST	AL1	AL1	DKF	DKF	AL1			

REFERENCE Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 436) no sapiens sapiens (human) Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. EST 04-SEP-2003 cDNA clone

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RESULT 2
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                                           AUTHORS
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488 bp mRNA linear EST 29-JAN-19
af76d07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1047949
5' similar to SW: SP17_HUMAN Q15811 SH3 DOMAIN-CONTAINING PROTEIN
1 (bases 1 to 488)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geise Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J., Moore,B., Schellenberg,K., Steptoe,M.,
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              Homo sapiens
                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No sl sequence available. This clone (DKFZp762K055) Please contact the RZPD: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
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Contact: MIPS
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                                                                                                                                                                                                   ; contains Alu repetitive element;, mRNA sequence.
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/db_xref="eaxon:9606"
/clone="DKFZD762K055"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="762 (synonym: hmel2)"
/note="Vector: pSport1; Site_1: Not1;
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Ressourcenzentrum, Heubnerweg 6, 140
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Matches:
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                                 Dubuque, T., Geisel, G.,
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RESULT 3
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JOURNAL
COMMENT
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Best Local Similarity:
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                                           AA773263
489 bp mRNA linear EST 29-JAN-1:
af82e11.rl Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:104855:
5' similar to SW:SP17_HUMAN Q15811 SH3 DOMAIN-CONTAINING PROTEIN
                 SH3P17. ; contains Alu repetitive element;, mRNA sequence
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AA773263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
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Location/Qualifiers
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314 286 1810
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/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Pollowing HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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pregnant uterus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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1 (bases 1 to 489)
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4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Wilson RK
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//clone lib="Soares NhHMPu S1"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.B. clones 260232-265223,
34048B-345479, and 48448B-489479."
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pregnant uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,
and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-(
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Computer-based methods for the mouse full-length cDNA concelopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
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Tel: 81-45-503-9222
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/strain="C57BL/6J"
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/cell_type="melanocyte"
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Plate: K0934 row: C column: 04
Seq primer: -21M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      בשגמדyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 573)
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K0934C04-5N NIA Mouse Neural Stem Cell
Library (Long) Mus musculus cDNA clone
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institute on Aging/National Insti
333 Cassell Drive, Suite 4000, Baltimore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Systematic Analyses of NIA Mouse Neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA=No.
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quality sequence stpp: 573
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                                                                                                                                                                                                                                                             /clone lib="NIA Mouse Neural Stem Cell (Undifferentiated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon|:10090"
/clone="NIA:K09b4C04 IMAGE:30087483"
                                                                                                                                                                                                                                                                                                                                                                  /db_xref="niaEST:K0934C04-5N"
                                                                                                                                                                                                                                                                                                                                                                                      strain="CD1"
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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more, MD 21224-6820, USA
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(Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN

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RESULT 6
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COMMENT
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
                                                                                                                                                                                                                                                                                                                                                                              Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komo, M., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, X., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIXEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 bp mRNA linear EST 26-OCT-2001
BB656585 RIKEN full-length enriched, 12 days embryo spinal ganglion
Mus musculus cDNA clone D130043E15 5', mRNA sequence.
BB656585
                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                 Tel: 81-45-503-9222
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                       1 ValLysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                           ThrIleGlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrp
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                                     CCA 190
                                                                         Pro 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rik
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spinal_ganglion"
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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                                                                                           KEYWORDS
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Best Local Similarity:
Query Match:
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                           382 ACTATCCAGCCAGGAGACATAGTCATGGTGGATGAAAGCCAAACTGGAGAACCCGGCTGG
                                                                                                                                                                                                                                                                                                                     61 Pro 61
                                                                                                                                                                                                                                                                                                                                                                                      41 LeuGlyGlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 657)
Hegde, P., Qi, R., Abernathy, K., Dha
Holt, I.E., Saeed, A.I., Sharov, V.,
                                                                                                                                      CF737796 698 bp mRNA linear UI-M-HDO-ckt-i-l1-0-UI.rl NIH BMAP_HDO Mus musculus IMAGB:30611818 5', mRNA sequence.
CF737796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: John Quackenbush
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST362129 MAGE resequences, MAĞA Homo sapiens cDNA, AW950164
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: johnq@tigr.org
Plate: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quackenbush,J.
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                                                        Mus musculus
                                                                           Mus musculus (house
                                                                                                                   CF737796.1
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malia; Eutheria;
(bases 1 to 698)
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j. .657
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/note="Vector: pBluescriptSKm"
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                                                                             mouse)
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Conservative:
Mismatches:
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US-09-720-934-2_COPY_740_800 (1-61)
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      ACCESSION
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                                                                                                                               BC062938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 GTAAAAGTGGTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATC
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                            Mus musculus intersectin (SIMAGE:6839463), containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                         BC062938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: pYX-5.
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Tissue Procurement: Dr. James
cDNA Library preparation: Di
                                                                                                                                                                                                                         CCA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATCCAGCCÁGGAGATATAGTCÁTGGTGGÁTGAAAGCCAGÁCTGGÁGAGCCAGGATGG 359
                                                                                                                                                                                                                                                                                                                                               CTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATT 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer containing a Not I site .Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx.Asc vector. The library tag sequence located between the Not I site and the polyA tail is TRATTGAACT. This library was created for the University Iowa Brain Anathmy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BNAP_HD0"
/clone_lib="NIH_BNAP_HD0"
/clone_Torgan: Eye; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
grine first strand_cDNA synthesis was primed with oligo-dT
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                                                            5385 bp
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                               SH3 domain protein 1A), mRNA (cDNA clone frame-shift errors.
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Indels:
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                                                                                      Alignment Scores:
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      Best Local Similarity:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kordrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A. Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and intilal analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Series: Plate: Row: Column: 0
This clone has the following problem: frame shifted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1. .5385
                                                                                                                                                                                                                                                                            tissue_type="Brain"
/clone_lib="NIH_BMAP_GHO"
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                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"/
                                                                                                                                                                                                                                                     lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:6839463"
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Dr. James Lin, Universtiy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City,
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ValLysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordinated Laboratory for Computational Genomics
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
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             /strain="Sprague-Dawley"
/db xref="Laxon:10116"
/clone="UI-R-FJO-Cpy-m-13-0-UI"
/tissue type="embryo"
/dev_stage="embryo"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-FJO"
/clone_lib="UI-R-FJO"
/note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
/UI-R-FJO is a cDNA library containing the following
tissue(s): rat embryo. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
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                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           type="mRNA"
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  cDNA was ligated
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with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT).18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 ATCCAGCCAGAGATATAGTCATGGTGGATGAAAGCCAGACCGGAGAGCCAGGATGGCTT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 703)
1 (bases 1 to 703)
                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
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UI-M-FY0-cfh-m-16-0-UI.rl NIH_BMAP_FY0 Mus
IMAGE:6849689 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                 Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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National Institutes of Health,
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                                                                                                                                                                                                                                                                                 primer: pYX-5
                                                                                                                                                                                                                                                                                                                         is clone was contributed by the
                /tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                              /db_xref="taxon:10090"
                                                                                                                                       clone="IMAGE:6849689"
                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                           ocation/Qualifiers
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  Soares,
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Research, 6:791-806
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DB:
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                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 673)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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CF735070.1
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                                                                                                                                                   Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                 (BMAP)
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                          /mol_type="mRNA"
/strain="C57BL/6"
db_xref="taxon:10090"
                                                                        organism="Mus musculus"
                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 443)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA492783
443 bp mkNA linear bol 20-000.
vi77g07.r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE:918300 5', mRNA sequence.
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     AA492783.1
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                                                                                                                               The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_tib="NIH_BMAP_HB0"
/note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                          CF738758 600 bp mRNA
UI-M-HDO-cku-c-22-0-UI.rl NIH BMAP HDO Mus
IMAGE:30610533 5', mRNA sequence.
CF738758
CF738758.1 GI:37635095
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:530516
                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                            EST
                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28ml3 revl ET from Amersham
                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrIleGlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCCCTGCAAACTATGCAGAAAAGATT
                                                                                                                                                                                                                                                          musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="SOLR (kanamycin resistant)"
/clone lib="Stratagene mouse testis (#937308)"
/clone="Ib="Stratagene mouse testis (#937308)"
/note="Organ: testis; Vector: pBluescript SK-; Site_1:
BCoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="10-12 week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="males"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CD-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus
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98.36%
96.72%
95.20%
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Indels:
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                                                                                                                                                                                                                                                                                                                                                        musculus
                                                                                                                                                                                                                                                                                                                                                                          linear
                                            Iowa
University of Iowa
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                            of Iowa
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REFERENCE
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ORGANISM
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Best Local Similarity:
                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                     AV669700
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-720-934-2_COPY_740_800 (1-61) x CF738758 (1-600)
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                                                                                                                                                                                                                                                                             ACCESSION
     AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 GlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIlePro
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                                                                                                                                                                                                                                                                                                                         AV669700 AV669700 OLHNI cell line cDNA library (OLb) Oryzias latipes cDNA clone OLb10.07g similar to adaptor protein intersectin (African
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neorteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 551)
                                                                                                                                                                    Oryzias latipes (Japanese medaka)
Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
Naruse, K., Tanaka, M., Shima, A. and Mitani, H
Medaka EST Project in University of Tokyo
                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                               clawed frog), mRNA sequence.
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This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                   AV669700.1
                                                                                                                                                                                                                                                                             AV669700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATGGCTTGGAGGAGAGCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleValMetValAspGluSerGlnThrGlyGluProGlyTrpLeuGlyGlyGluLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIleGlnProGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DHIOB (TI phage resistant)"
/clome lib="NIH BMAP HDO"
/clome lib="NIH BMAP HDO"
/note="Organ: Eye; Vector: pyx- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev_stage="embryo_12.5,13.5,14.5 dpc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="whole eye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:30610533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain="C57BL/6"
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                                                                                                                                                                                                                                                     GI:9935498
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100.00%
90.69%
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arch com b time :	Qy da	Qу ДЬ 21	Qy :	Qу рь 1	US-09-720-93	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	COMMENT FEATURES Source ORIGIN
leted: July 1, 2004, 19:48:42 1843 secs	61 Pro 61 341 CCG 343	41 LeuGlyGlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle 60	21 ThriledinProGlyAspileValMetValAspGluSerGlnThrGlyGluProGlyTrp 40 :::	1 VallysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle 20	720-934-2_COPY_740_800 (1-61) x AV669700 (1-551)	Cores: 1.46e-27 Length: 551 301.00 Matches: 51 Conservative: 9 Similarity: 83.61% Mismatches: 1 90.39% Indels: 0 Gaps: 0	Contact: Kiyoshi Naruse Department of Biological Sciences Graduate School of Science, University of Tokyo Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan Tel: 81-3-5841-4443 Fax: 81-3-5841-4440 Bmail: naruse@biol.s.u-tokyo.ac.jp This clone was isolated from OLHNI cell line cDNA library (OLb) 5' end sequences. 1551 //organism="Oryztas latipes" //mol_type="mgNA" /strain="HNI" /db_xref="taxon 8090" /clone="OLD10.079" /clone="OLD10.079" /clone="OLD10.079" /clone="OLD10.079" /clone=lib="OLHNI cell line cDNA library (OLb)"

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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US09720934/runat_30062004_064539_13430/app_query.fasta_1.1386
-Q=/cgn2 1/USPTO_spool_p/US09720934/runat_30062004_064539_13430/app_query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SUFFIX=xge -MINWATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 = END0=-1 -MATRIX=bitseum62 -TRANS=human40.dd -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09720934 @GCN_1 1_7509 @runat_30062004_064539_13430 -NCFU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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           3470272 seqs,
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gb_ro:*
gb_ro:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21671516995 residues
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_other:*
32: em_htg_other:*
33: em_htg_pln:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_wrt:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_num:*
41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 3231)

E Korenberg, J. R. and Chen, X.N.

Isolated SH3 gene relating to myeloproliferative disorders and leukemia and utilization thereof leukemia and utilization thereof
Patent: JP 2002511267-A 5 16-APR-2002;
CEDARS SINAI HEALTH SYSTEM ET AL

HOMO sapiens (human)
PN JP 2002511267-A/5

PD 16-APR-1999 US 60/082007

PI JULIE R KORENBERG, XIAO NING CHEN
C1201/69, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
PC C1201/69, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
PC G1N33/68/A61K48/00, C12N15/00, C12N5/00

CC Isolated SH3 gene relating to myeloproliferative disorders and
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Isolated SH3 gene relating to myeloproliferative disorders and
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Chordata;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                   Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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AF03211B.1 GI:2642624
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Cloning of ligand targets: systematic isolation domain-containing proteins
Nat. Biotechnol. 14 (6), 741-744 (1996)
1 (bases 1 to 4103)
Yamabhai, M., Hoffman, N.G.,
Castagnoli, L., Cesareni, G.
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Submitted (18-JUN-1996) CYTOGEN
Princeton, NJ 08540, USA
                                                     Xenopodinae; Xenopus.
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KGKTGWFPANYAEKIPENEVPAPVKPVTDSTSAPAPKLHETPAPLTSSEPSTF
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STALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLFPSNY
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Direct Submission
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ESTINKSRELRIAE ITHLOQLOESOOLLGKMI PEKGSLI DOLKQVQONSLHRDSLLTL
KRALETKEI GRQQLRODLEVEKETRAKLOEI DV FNNOLKELRELYNKQOFGKQODE
TEKI KOKELERKTSELDKLKERDKRAMLEODKLWODRVKGEERRYKFODEEKEKREES
VOKCEVEKKPEI GEKPINKEP FHQP PEPGKLGGGLKWODRVKGETRYNTONCVESDEWDT
YFFDARSHDEITI EPGDI I MVDESQTGEFGMLGGELKGKTGWF FANYAERNEESEPS
TTKRAAETTAKPTUHVARSVYARAATNITSTNSNNWADFSGTWFTINNTOKVESDEWDT
WAAQPSLTVPSAGQHRORSAAFTRTSTNSNNWADFSGTWFTINNTOKVESDEWDT
WAAQPSLTVPSAGQHRORSAAFTRTSTSS PSPVLGQGEKVEGLOAGALYPWRAKKDN
HLNENKUDVITVLEQODMWWFGEVGGOKGWF PKSYVKLISGFLEKSTSIDSTSSESPA
SLKRVSSPARKPAI QGEEY I SMYTYBSNEGGILTFOQGELI VVI KKDGDWMTGTVGEK
TGVFPSNYVRP KDSEAAGSGGKTGSLGKKPEI AQVIASYAATAPEQLTILAFGQLITA
KKNPGGWMEGELQARGKKROI GWFPANYVKLISPTTBEP KRTSLFTCOVIG
KKNPGGWMEGELQARGKKROI GWFPANYVKLISPTTBEPKFTSLPFTCOVIG
KKNPGGWMEGELQARGKKROI GWFPANYVKLISPTTBEPKFTSLPFTCOVIG
KKNPGGWMEGELQARGKKROI GWFPANYVKLISPTTBEPKFTSLFTCOVIG
MYDYI AQNIDDELAFSKGQVINVLNKEDPDWWKGELNGHYGLFBSNYVKITTDMDFSQO
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/note="EH domain and SH3 domain containing protein;
similar to intersectin binding proteins Ibp1, encoded by
GenBank Accession Number AF057285, and Ibp2, encoded by
GenBank Accession Number AF057286, and mouse
Rab/Rip,encoded by GenBank Accession Number AF057287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / translation="MAQFGTPFGGNLDIWAITVEERAKHDQQFHGLKPTAGYITGDQA
RNFFLGSGLPQPVLAQIWALADMNNDGRMDQLEFSIAMKLIKLKLQGYPLBSIISHSIN
LKQPVAMPAAVAGFGMSGIVGIFPLAAVAFVEMPSIFVYGMSPELVSVETVPPLSN
GAPAVIQSHPAFAHSATLPKSSSFGRSVAGSQINTKLQKAQSFDVPAPPLVVEWAVPS
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EFILAMHLIDVAMSGQPLPPILPPEYIPPSFRRVRSGSGLSIMSSVSVDQRLPEEPEE
                                                                                                                                                                                                                                                    3607.
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3364...3558
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3148. .3324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="intersectin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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BX538175
BX538175.1 G
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686J17173) is available at the RZPD in Berlin.
This clone (DKFZp686J17173) is available at the RZPD in Berlin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please contact the RZPD: Ressourcenzentrum, Heubnerwe Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de information about the clone and the sequencing projections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lauber, J., Bahr, A., Mewes, H.W., Fobo, G., Han, M. and Wiemann, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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Location/Qualifiers
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PSFRRVRSGSGISVISSTSVDQRLPEEPVLEDEQQOLEKKLPVTEDKKRENFERGNL
PSFRRVRSGSGISVISSTSVDQRLPEEPVLEDEQQOLEKKLPVTEDKRENFERGNL
                                                                                                                                                                                                                                                                                                                                                                                                /note="intersectin long
differentially spliced"
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QERDKQWLEHVQQEDEHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLGRLFHQ
HQEPAKPAVQAPWSTAEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMV
                                                                          ELEKRROALLEOORKEOERLAOLERAEOERKEREROEOERKROLELEKOLEKORELER
OREEERKE ERREAKRELEROROLEWERRERELLNORNKEOED I VVIKAKKKTIE
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LGRLI PEKOI LNDOLKOVOONSLHRDSLVTLKRALEAKELAROHLRDOLDEVEKETRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="human uterus endothel primary cell culture"
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DH10B; sites SfiIA + SfiIB"
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/map="21q22.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DKFZp686J17173"
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                                      Pred. No.:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated SH3 gene relating to myeloproliferative dis leukemia and utilization thereof for the provided in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2409
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Isolated
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Korenberg, J. R. and Chen, K. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluValGlnGlyGlnLysGlyTkpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnPheAsnLysAsnAspVallheThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
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                                                                                                                                                                                                                                                                                                                                                               and utilization thereof.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1999 JP 2000543610
16-APR-1998 US 65/082007
JULIE R KORENBERG, XIAO NING CHEN
C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
                                                                                                                                                                                                                                                                               /organism='Homo sapiens
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4267. .4272
/gene="DKFZp686J17173"
4289
                                                                                                                                                    /organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon;9606"
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o myeloproliferative
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disorders and
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RESULT 6
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Query Match:
                                                                   US-09-720-934-2_COPY_908_966 (1-59) x BD205033 (1-5199)
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                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 5199)
Korenberg, J.R. and Chen, X.N.
Isolated SH3 gene relating to myeloproliferative leukemia and utilization thereof patent: JP 2002511267-A 1 16-APR-2002; CEDARS SINAI HEALTH SYSTEM ET AL
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Isolated
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JP 2002511267-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD205033
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                      ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu 20
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 GTGGAGGGGCTACAAGCTCAAGCCCTATATCCTTGGAGAGCCAAAAAAGACAACCACTTA 2988
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                                                                                                                                                                                                                                                                                                                                                                                              and utilization thereof.
Location/Qualifiers
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16-APR-1998 US 60/082007
JULIE R KORENBERG,XIAO NING CHEN
C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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JP 2002511267-A/1
16-APR-2002
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                                                                                                                                                                                                                                                                                                                                           /organism='Homo sapiens (human)'
Location/Qualifiers
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                    4.45e-37
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o myeloproliferative
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-MAY-1998) Genetics
Michel-Servet, Geneva 4 CH-1211,
Location/Qualifiers
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1 (Dases 1 to 5287)

Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guipponi, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens intersectin short form AF064243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antonarakis,S.E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSALPPVMKQQPVAISSAPPFGMGGIASMPPLTAVAPVPMGSIPVVGMSPTLVSSVETAAVPPLAN
                                                                                                                               VTKKDGDWWTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYTAT
GPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLNPGTSKITPT
                                                                                                  eppkstalaavcqvigmydytaqnddelafnkgqiinvlnkedpdwwkgevngqvglf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
product="intersectin short form"
protein id="AAC78610.1"
/db_xref="GI:3859853"
                                                                                PSNYVKLTTDMDPSQQ"
                                                                                                                                                                             IRKSTSMDSGSSESPASLKRVASPAAKPVVSGEEFIAMYTYESSEQGDLTFQQGDVIL
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott, H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5287 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Microbiology,
Switzerland
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                                                                                                                                                                                                                                                                   Pucharcos,C., Fuentes,J.J., Pritchard,M. and Estivill,X. Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center, Cancer Research Institute, I'Hospitalet de Ilo., Avia. Castelldefels km. 2,7, Barcelona 08907, Spain Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Allusplice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                   269. .393
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                       /gene="ITSN"
                                                                                                                  /map="21q22.1-q22.2"
                                                                                                                                                                                               organism="Homo sapiens"
|mol_type="mRNA"
codon_start=1
                                                                           'gene="ITSN"
                                                                                                                                                 chromosome="21"
                                                                                                                                                                           'db_xref="taxon:9606"
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Euteleostomi;

Alcantara,

complete cds. PRI 16-JUL-2002

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KEYWORDS
SOURCE
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidde; Homo.
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JP 2002511267-A/2.
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EEFILAMHLIDVAMSGQPLPPVLPFEYIPPSFRRVRSGSGISVISSTSVDQRLFEEPV
LEDEQQQLEKKLPVTFEDKKRRWFERGNLELEKRRQALLEQQRKEGERAAQLERAEQE
EKERERQEQERKRQLELEKQLEKQRELERQREBERRKEIERRAAKRELERQRQLEME
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SH3 gene relating to myeloproliferative disorders and
and utilization thereof.
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EIESTINKSREIRI JAEŢTHLQQQLQESQQMCIGRLIFENGLKUCKQVQQNSLIRDSIV
TLKRALEAKELARGHLRODLDBVEKETTSKLOBID FENGLKELERIHKQQLQESQQMCIGHLIFENGLKELREIHKQQLQEDGKY
MEAERLKQKEGERKIŢELEKQKEEAQRRAQERDKQMLEHVQQEDEHQRPRKLHEEEKI
KREESVEKKDGEEKGKQBAQDKLGRLFHQHQEDAKPAVQAPMSTABKGPLTI SAQENV
KVVYYKALYPEPESRSHBDETIQPGDIVMVKGBWDDESQTGEPGWLGGELKGKTGWFPA
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EIGAQALYPMRAKKDWHLHFNKNDUTŢVLEQDDMWFGEVGGOKGWFPKSYVKLISGS
FIRKSTSMDSGSSESPĀSIKKRVASPAAKPVVSGEEFIAMYTYESSEQGDLTFQQGDVIL
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EPPKSTALAAVCQVI$MYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF
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/protein_id="AAP29953.1"
/db_xref="GI:4808825"
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1 (bases 1 to 6439)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M.

Alu-splice cloning of human Intersectin (ITSM), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                               Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
Cancer Research Institute, L'Hospitalet de Llo., Avia.
Castelldefels km. 2,7, Barcelona 08907, Spain
Location/Qualifiers
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Pucharcos,C., Fuentes,J.J., Pritchard,M. and Estivill,X.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
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CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKWNSNCQFFIRDLEQEVLCITVFERDQ
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
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/protein_id="AAD29952.1"
/db_xref="GI:4808823"
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EPFKSTALAAVCQVIGWYDYTAQNDDELAFNKGGINHLEKEDBPWKGGWNGGVNGGIF
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PSNYVKLTTDWDPSQOWGDLHILDMLTPTERRROGYHLELIVTEBNYVMDLQLVETI
PGKPLMESELLTEKEVAMIFVNWKELLMCNIKLLKALRVRKMSGEMPVKMIGDILS
AQLPHMQPYIRFCSRQLMGAALIQKTDEAPDFKEFLKELEMDFPCKGMFLSSFILKF
MQRVTRYPLIINILSTENDENIPDHSHLKHALLEKAEELCSQVNBGVRKKENSDRLEN
DQHVQCEGLSBQLVFNSVTNCLGPRKFLHSGKLYKAKNNKELYGFLFNDFLLLTQITK
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GLQAQALYPWRAKKDHILNFNKNDVITVLEQODMWFGSVQGQKGWPPKSYVKLISGF
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LIKKSTSMDSGSSESPASLKKVASPAAKPVVSGEBFIAMYTYBSSEQGDLTFQQGDVIL
VTKKDGDWWTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYTAT
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KVVYYRALYPFESRSHDEITIQPGDIVMVKGEWVDESQTGEPGWLGGELKGKTGWFPA
NYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTPNNWADFSST
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EIESTRKSRELRIAEITHLOQOLQESQOMLGRLÍPKOLINDOLKOVOONSLHRDSIV
TLKRALEAKELARGHLRODLDEVEKTTRSKLOBIDIRNOLKELREIHNKOOLOOKS
MEAERLKOKEQERKIIELEKOKEEAQRRAQERDKOMLEHVQQEDEHORPRKLHEBEKL
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                                                          FSPDDFLGRTEIRVADIKKDQGSKGPVTKCLLLHEVPTGEIVVRLDLQLFDEP"
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LEDEQQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQE
                                                                                      CRSHGKSNPYCEVIMGSQCHITKTIQDTLNPKWNSNCQFFIRDLEQEVLCITVFERDQ
                                                                                                               AESINERTAWVQKIKAASELYIETEKKKREKAYLVRSQRATGIGRLMVNVVEGIELKP
                                                                                                                                                 PLGSSGTDKVFSPKSNLQYKMYKTP1FLNEVLVKLPTDPSGDEP1FH1SH1DRVYTLR
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/note="encodes EH domain"
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/tissue_type="brain"
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SOURCE
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                                                                                                                                                                                                                                                                                                     Submitted (26 MAY-2003) Shengyue Wang, Chinese National Human Genome Center at Shanghah, Genomic Sequencing; No.250 BiBo Road, Zhang Jiang HI-TECH Park, Shanghai 201203, CHINA (E-mail:wangsy@chgc.sh.ch, URL:http://www.chgc.sh.cn, Tel:86-21-50801919, Fax:B6-21-50801922)
The Chimpanzee Chromosome 22 Sequencing Consortium consists of: *Chinese National Human Genome Center at Shanghai, Shanghai, China; *Chinese National Human Genome Center at Shanghai, Shanghai, China; *Chinese National Human Genome Center at Shanghai, Shanghai, thina; *GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 52814)
Wang,S., Cai,Z., Wang,B.,
Lu,G., Fu,G. and Chen,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences, complete sequence.
BS000183
BS000183.1 GI:37537450
               Contact: wangsy@chgc.sh.cn
----- Project Information
Center project name:The Chimpanzee
Center clone name: PTB-086H16
                                                                                                                                          Center: Chinese National Human Genome Center at Shanghai Center
                                                                                                                                                                                                                         Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*Maxional Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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DNA sequence of chimpanzbe chromosome 22 and its ev
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                                                                                                  Web site:
                                                                                                                                                                  *RIKEN Genomic Sciences Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluValGlnGlyGlnLysGlyTtpPheProLysSerTyrValLysLeuIleSerGly 59
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                                                                                                  http://chgc.sh.cn
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Summary
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che 22 clone:PTB-086H16, map
Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                   Yokohama, Japan
                                       Chromosome
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22, partial
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RESULT 13
AP000193
LOCUS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                       21 AsnPheAsnLysAsnAspValIleThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
AP000193
AP000193.1
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: pUC18,100% of reads Chemistry: Dye-terminator Big Dye and ET; 100% program: Phrap; version 0.990329 Consensus quality: 52712 bases at least Q40 Consensus quality: 52814 bases at least Q30 Consensus quality: 52814 bases at least Q30 Consensus quality: 52814 bases at least Q30 Consensus quality: 52814 bases at least Q20
                                                                              Homo sapiens genomic DNA, clone Q78C10-f32E9, segmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This entry has been annotated with sequence estimates computed by the Phrap assembly program. estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 9.2x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neighboring clones: PTB-301D17(left) and RP43-082007(right)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones may be obtained from Asao Fujiyama and (http://www.gsc.riken.go.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source information:
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                                                                                                                                                                                                                                                                                 GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAGGGGCTACAAGCTCAAGCCCTATATCCTTGGAGAGCCAAAAAAAGACAACCACTTA 43348
                                                                                                                                                                                                                                            GAAGTTCAAGGTCAGAAGGGTTGGTTCCCCCAAGTCTTACGTGAAACTCATTTCAGGG 43465
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/clone_lib="PTB1 chimpanzee BAC"
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/db_xref="taxon:9598"
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nme 21q22.1, D21S226-AML
complete sequence.
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RESULT 14
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        1 (bases 1 to 114929)
Hattori,M., Ishii,K., Toyo
Homo sapiens genomic DNA,
                                                                                                                                                                                                                                                                                                              AP000050 114929 bp DN Homo sapiens genomic DNA, chromosome
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              Homo sapiens
                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                               AP000050.1 GI:3132360
                                                                                                                                                                                                                                                               AP000050
                                                                                                                                                                                                                                                                                 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the insertion and genomic sequences experimentally, removed the insertion sequences, reconstituted the present data. The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)

E. coli transposon insertion:The present data does not contain leads to the contain 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10000)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.

Homo sapiens 2,083,744bp genomic DNA of 21g22.1 (REGION: D21S226-AML CLONE RANGE: Q78010-f32E9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli transposon insertion: The present data does not contain coli transposon sequences which integrated in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             original/previous sequences. We determined the boundary between
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2 (bases 1 to 100000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTTTAACAAAATGATGTCATCACCGTCCTGGAACAGCAAGACATGTGGTGGTTTGGA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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        Toyoda,A., Shiba,T. and Sakaki,Y. DNA, chromosome 21q
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Matches:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 125242)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-S Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y. Homo sapiens 125,242bp genomic DNA of 21q22.1
Published Only in DataBase (1999)
2 (bases 1 to 125242)
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This sequence is conducted by Kitasato University JST sequencing Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5522, Fax: +81-3-5449-5445, sakaki@hgc.ims.u-tokyo.ac.jp
Sub-leader: Taddyoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by:Human Genome Sequencing in ALIS project of the sequence of the submitted by:Human Genome Sequencing in ALIS project of the sequence of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS project of the submitted by:Human Genome Sequencing in ALIS proj
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2 (bases 1 to 114929)
Hattori,M., Ishii,K., Toyoda,A.,
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Toyoda, A., Taylor, T.D.,

Hong-Seog, P.,

Direct Submission Direct Submission Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Majan (E-mail:hattoriogsd.riken.go.]p, Tel:81-42-778-9923), Fax:81-42-778-9924) The sequence is a part of the data (ACCESSION No. AP000174 - AP000194). The sequencing project is supported by Japan Science Technology (Corporation (GST) and The Institute of Physical and Chemical 10.12542 [Accession (Joualifiers 10.12542 Jouanisms Homo Eaplens Jo	Search completed: July Job time : 1396.81 secs	Qy 41 Db 109587	Qy 2: Db 10952	Qy :	US-09-720-93	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB:	ORIGIN	source	FEATURES		T L	ΑĽ	H HILLI
20 109526 109586	-	GluValGlnGlyGlnLysGlyTkpPheProLysSerTyrValLysLeuIleSerGly	21 ASNPheASNLYSASNASDVallieThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40 	1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu 20 	US-09-720-934-2_COPY_908_966 (1-59) x AP000311 (1-125242)	1.63e-35 Length: 328.00 Matches: y: 100.00% Conservative: 100.00% Mismatches: 100.00% Indels: 9 Gaps:			Location/Qualifiers	AP000194). The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).	Japan (E-mail:hattoriwgsd.riken.go.]p, URL.http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)	Submitted (13-MAY-1999) Wasahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,	Fujiyama,A., Yada,T., Todoki,Y. and Sakaki,Y.

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-Q=/cgn2_1/USPTO_spool_p/US9720934/runat_30062004_064540_13455/app_query.fasta_1.1386
-DB=Issued_patents_NA -QPMT=fastap_-SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-DOPEXT=0-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPENCOK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARM_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6
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US-08-630-915A-193

US-09-833-381-1294

US-09-620-312D-676

US-09-620-312D-675

US-10-164-595-17

US-10-164-595-21

US-10-164-595-19

US-08-942-423-68

US-08-942-423-68

US-08-630-915A-25

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 Sequence 193, App
Sequence 1294, App
Sequence 676, App
Sequence 675, App
Sequence 17, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 17, Appl
Sequence 25, Appl
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Sequence 1396, Appl
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Sequence 49, Appl	equence 2,	ຸ້	, Appl	1,	123	3,	3, Appl	equence	e 1,	equence 1, Appl	equence 5,	equence 37	e 20	equence 19	equence 1, 🌶	equence 13	equence 1, App	equence 79, F	equence 48, F	e 65	equence 931,	equence 1,	e 1, Appl	e 1, Appl	equence 1, Appl	equence 1, Appl	equence 3,	equence 3, Appl	æ	equence 3, Appl	Sequence 39, Appl

ALIGNMENTS

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RESULT 1
US-08-630-915A-193
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APPLICANT: SPARKS,
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCONNELL
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                     ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                              STREET:
CITY: N
                                                                                                        APPLICATION NUMBER: FILING DATE: 03-APR CLASSIFICATION: 536
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                   MCCONNELL, Stephen J.
VENTION: POLYPEPTIDES HAVING A FUNCTIONAL
VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAY, Brian K. FOWLKES, Dana M.
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                                                                                                                                                                                                                                                                                                                                                                  Pennie &
                                                                                                              03-APR-1996
N: 536
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                                       18,872
ER: 1101-174
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DB:
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Verbion
SEQ ID NO 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1294, Application US/09833381
Patent No. 6672186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 970
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                         No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: unknown
                                                         316
                                                                                                                         376 AAGGCCTTGTATTCTTTTCAAG¢CAGGCAAGATGATGAGTTGAATTTGGAAAAGGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GluValGlnGlyGlnLysGlyTkpPheProLysSerTyrValLysLeuIleSerGly
                       46
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                                                                                                                                                       7 GlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsnPheAsnLysAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu 20
LysGlyTrpPheProLysSerTyrValLys 55
                                                   ATTGTGATTATACACGÁGAAAAÁAGAAGAAGGATGGTGGTTTGGÁTCTTTGAATGGGAAA 257
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129.50
74.00%
42.00%
39.48%
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251.00
86.44%
74.58%
76.52%
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Matches:
Conservative:
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Matches:
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Query Match:
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                                                                                                                                                                                                                                                                          Percent Similarity:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2955)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (169)..(2418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                              1678
1738 GGCCTGCGAGGCTGGTTTCCAGCCAAGTTCGTGGAAGTCCTG 1779
                                                                                                                            1618 CGAGCCAAGGCCTGCTGGACTTTGAGCGGCACGACGACGACGAGCTGGGCTTCCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                          44 GlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIle 57
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                                                                                          25 AsnAspValileThrValLeuGluGlnGlnAsp---MetTrpTrpPheGlyGluValGln 43
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                                                                                                                                                         5 GlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsnPheAsnLys 24
                                                              Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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125.50
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40.74%
38.26%
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; Sequence 675, Application US/09620312D

US-09-620-312D-675

Patent No. 6569662 GENERAL INFORMATION:

APPLICANT: Tang,

Chenghua

Vinod

APPLICANT: APPLICANT:

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Query Match:
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US-09-620-312D-675
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Patent NO. THORMATION:
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
                                                                                         Sequence 17, Application Patent No. 6657054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317
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PRIOR FILING DATE: 2000-01-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                      1822 GGCCTGCGAGGCTGGTTTCCAGCCAAGTTCGTGGAAGTCCTG 1863
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                                                                                                                                                                                                                                                                                                                     5 GlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsnPheAsnLys
                                                                                                                                                                                             GlyGlnLysGlyTrpPheProLysSerTyrValLysLeuile 57
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhang, Jie
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Xue, Aidong J.
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Wehrman, Tom
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n, Rui-hong
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22 PheAsnLysAsnAspValIleThrValLeuGluGln---GlnAspMetTrpTrpPheGly 40

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
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CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
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NAME/KEY: CDS
LOCATION: (264)..(3482)
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LOCATION: (264)...
CTHER INFORMATION:
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TYPE: DNA
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ORGANISM: Homo sapiens
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3303 AAGGGGAAGGCCAAAGCCTTATATGATTTCCGAGGGGAAATGAAGATGAACTTTCC
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                                 2 GluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsn
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RESULT 7 US-10-164-595-19

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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: US-10-164-595-19
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Patent No. 6657054
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Patent No. 5891673
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TITLE OF INVENTION: Regulated Angiogenesis Genes
FILE REFERENCE: 1U 103 R1
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2002-06-10
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                                                                                                                                                                                                                                                        APPLICANT: Takemoto, Yoshihiro TITLE OF INVENTION: Lck Binding NUMBER OF SEQUENCES: 68
SOFTWARE: PatentIn Release #1.0,
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                   STREET: 3401 Hilly
CITY: Palo Alto
STATE: California
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                                                                                                                                       U.S.A.
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Temoto, Yoshihiro
                                                                                                                                                                                             Syntex (U.S.A.)
01 Hillview Ave.
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08942423
Patent No. 5891673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1698
TELEPAX: (415) 496-3529
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/362,715
FILING DATE: 23-DEC-1994
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MOLECULE TYPE:
                                                           APPLICATION NUMBER: US/08/942,423
FILING DATE: 01-0CT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
  APPLICATION NUMBER: US 08/362,715 FILING DATE: 23-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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CTTY: Palo Alto
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                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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VENTION: Lck Binding Protein
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                                                                                                                                                                                                                                                                                   U.S.A.
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Percent Similarity:

Alignment Scores:

SEQ ID NO 19 LENGTH: 5581

TYPE: DNA

FEATURE: NAME/KEY: CDS

US-08-942-423-68

APPLICANT:
APPLICANT:

COUNTRY:

94303

ADDRESSEE:

Peries, Rohan

28260

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RESULT 10
US-08-630-915A-25
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TELEFAX: (415) 496-3529
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1698
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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              APPLICATION NUMBER: FILING DATE: 03-APR
                                                                                                                                                                                                CITY: New York
CLASSIFICATION:
                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                 ADDRESSEE:
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1155 Avenue of the Americas
                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                 KAY, Brian K.
FOWLKES, Dana M.
McCONNELL, Steph
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POLYPEPTIDES HAVING A FUNCTIONAL
DOWALN OF INTEREST AND METHODS OF IDENTIFYING
USING SAME
                                                           Release #1.0, Version #1.30
                          US/08/630,915A
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Matches:
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Best Local Similarity:
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Patent No. 6607879
GENERAL INFORMATION:
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                                                                                APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cocks, BOAPPLICANT: Susan G. APPLICANT: Jeffrey
                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
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                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                               COUNTRY:
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REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                     CITY:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1471 TGCCGTGGCCACTTTGGACTTTCCCTGCAAACTATGTCAAGCTCCTC 1518
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PALO ALTO
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                                                                                                                                                                                                                                                                                                 USA
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US-09-023-655-1296
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1968 base pair
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                               FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1390 GATCCGGACGTAATCACTGACATTGAGATGGTGGACGAGGGCTGGTGGCGGGGACGT
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VENTION: POLYPEPTIDES HAVING A FUNCTIONAL
VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
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(650) 845-4166
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/08630915A
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APPLICANT: SPARKS
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            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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SEQUENCE
                                                                                 TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
REFERENCE/DOCKET NUMBER:
                                               TELEFAX:
                                                              TELEPHONE:
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10036-2711
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CHARACTERISTICS:
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                                                 3: (212)
(212) 86
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65.45%
41.82%
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POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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Alignment Scores:
   Percent Similarity:
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Query Match:
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                                                                                                                                                                                              TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3:
                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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CITY: E
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                                                                                                               TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear
                                                                                                                                                                                                                                                                           NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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Length:
Matches:
Conservative:
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Query Match:
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US-08-484-710-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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STREET: ...
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Louis Myers REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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766 AAAGTAATATTTCCATATGAGGCACAGAATGATGATGAATTGACAATCAAAGAAGGAGAT
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                                                                                                                                    Similarity:
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                              7 GlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsnPheAsnLysAsnAsp
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Matches:
Conservative:
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 825
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8

27 ValIleThrValLeuGluGlnGlnAspMet---

---TrpTrpPheGlyGluValGln 43

Search completed: July 1, 2004, 19:53:51 Job time : 46.3138 secs 44 GlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIle 57 826 ATAGTCACTCTCATCAATAAGGACTGCATCGACGTAGGCTGGGAAGGAGGTGAAC 885

B & B

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-C2/G972_1/USPTO_Spool_p/US09720934/runat 30062004_064541_13481/app_query.fasta_1.1386
-DB=Published_Applications_NA -QFMT=fasta_p_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -STATE1 = LND=-1 -MATRIX=blosum62
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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m2_6/ptodata/1/pubpna/US09S_EW_PUB.seq:*
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SUMMARIES
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1572.471 Million cell updates/sec
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ALIGNMENTS

US-09-864-761-30400

GENERAL INFORMATION:

Sequence 30400, Application US/09864761 Patent No. US20020048763A1

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APPLICANT: Penn, Sharron G.

APPLICANT: Annk, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR APPLICATION NUMBER: US 09/632,366
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Result No.

Score

Query Match Length DB

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Description

FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00667

FILING DATE:

2001-01-30

FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666

APPLICANT:

Hanzel, David K.

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Pred.
                                US-09-864-761-13834
Sequence 13834, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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Best Local Similarity:
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TRNGTH: 206
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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NUMBER OF SEQ ID NOS: 49117
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USOh/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USOh/00663
OR APPLICATION NUMBER: PCT/USOh/00663
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APPLICATION NUMBER: PCT/US01/00661
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FILING DATE: 2001-01-30
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Penn, Sharron G.
Rank, David R.
                                                                                                                                                                                                           AACTTCTCAAAACATGACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTTTGGG
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EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

EXPRESSED IN LONG, SIGNAL = 1.1

EXPRESSED IN LUNG, SIGNAL = 1

NT HIT: AF182198.1 EVALUE 1.00e-112

SWISSPROT HIT: Q15811, EVALUE 3.00e-23

SWISSPROT HIT: AW505025.1, EVALUE 1.00e-112
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Matches:
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Indels:
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Query Match:
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                                                                                                                      US-09-720-934-2_COPY_908_966 (1-59)
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence
SEQ ID NO 13834
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PRIOR FILING DATE: 2001-01-1
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: MAP TO AC008073.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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OR APPLICATION NUMBER: PCT/US01/00666
OR ETLING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00663
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DB:
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Best Local Similarity:
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US-09-879-957-193
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                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                      MOLECULE
SEQUENCE
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FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly
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US20020034755A1
                                                     ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
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TELEFAX: (212) 869-8864/9741
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US-09-764-875-176
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                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 125
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APPLICANT: Rosen et
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                  Prior application data removed - refer to NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed -
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                     TYPE: DNA
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                          LENGTH: 4210
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o. US20040018969A1
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Best Local Similarity:
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RESULT 7
US-10-264-049-887
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Publication No. US20040053282A1
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APPLICANT: Ogawa, Kaoru
APPLICANT: Nagasu, Takeshi
APPLICANT: Obayashi, Masaya
APPLICANT: Saito, Hirohisa
APPLICANT: Takahasi, Eiki
TITLE OF INVENTION: Method of Testing For Allergic
FILE REFERENCE: SHIMIZU-07907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/JPCh/08937
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: JP 2000-314093
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Hashida, Ryc
APPLICANT: Ogawa, Kaoru
APPLICANT: Nagasu, Take
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/398,885A CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (7)..(5052)
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                                                                                      41 GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly
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                                                             CAGGTGCATGGAGGAAGAGGATGGTTTCCCAAATCTTATGTCAAGATCATTCCTGGG 2826
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-833-381-1294
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
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                                                                                     SEQ ID NO 1294
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA13391
                                                                                                   PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
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LOCATION: (2063)...(2063)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals
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                                                             ENGTH: 970
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US-10-104-047-1655
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      Sequence 115, Application US/09764868
Patent NO. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
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LENGTH: 2539
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FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
RUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-764-875-324
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; LENGTH: 2803
; TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1249
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ORGANISM: Homo
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                      44 GlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIle 57
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GGCCTGCGAGGCTGGTTTCCAGCCAAGTTCGTGGAAGTCCTG 1025
                                                               GlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIle
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o. US20040018969A1
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US-10-037-270-676

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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Tillinghast, John
APPLICANT: Tillinghast, John
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERRNCE: 784C1F2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: Pt FL genes Version 1.0
SEQ ID NO 676
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-037-270-676
US-10-117-722-676
; Sequence 676, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
                                                                    RESULT 13
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2955
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Xue, Aidong J.
Yang, Yonghong
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Zhang, Jie
Ren, Feiyan
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Percent Similarity:
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Query Match:
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Sequence 675, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/486,725
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 676
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (169)..(2418)
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
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APPLICANT:
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
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                                                  Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wehrman, Tom
           Wang,
, Yunqing
ng, Dunrui
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APPLICANT:

Tillinghast,

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APPLICANT: Drmanac, Radoje T.

FITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and FITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/10/037,270

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-01

VINNEER OF SEQ ID NOS: 1104

SOFTWARE: pt_Genes Version 1.0

SEQ ID NO 675

LENGTH: 3039
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US-10-117-722-675
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                                      SOFTWARE: pt_FL_genes Version 1.0 SEQ_ID_NO 675
                                                                                                                                                                                                                                                                                                                                                              Sequence 675, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
                                                                         PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
                                                                                                                                                                                                        APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCIP
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT FILING DATE: 2002-04-04
CURRENT FILING DATE: 2002-04-04
TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(3039)
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NAME/KEY: CDS
                     ENGTH: 3039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AsnAspValileThrValLeuGluGlnGlnAsp---MetTrpTrpPheGlyGluValGln 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeuAsnPheAsnLys
                                                                                                                                                                                                                                                                                                                                         Liu, Chenghua
Asundi, Vinod
Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCTGCGAGGCTGGTTTCCAGCCAAGTTCGTGGAAGTCCTG 1863
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; LCCATION: (1)...(3039)
; OTHER INFORMATION: n = a,t,c
US-10-117-722-675
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       1822
                                                   1702 CGAĞCCAAGĞCCCTĞCTGGACTTTGAGCGGCACGACGACGACGAGGCTĞGGCTTCCGCAAĞ 1761
                         44 GlyGlnLysGlyTrpPheProLysSerTyrValLysLeulle 57
                                                                             25 AsnAspValIjeThrValLeuGluGlnGlnAsp---MetTrpTrpPheGlyGluValGln 43
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Search completed: July 1, 2004, 20:16:02 Job time : 188.007 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum
Maximum
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-MODEL-frame+ pln.model -DEV=xlp
-MODEL-frame+ pln.model -DEV=xlp
-Q=(cgn2 1/USPTO_spool p/US09720934/runat 30062004_064540_13442/app_query.fasta_1.1386
-Q=(cgn2 1/USPTO_spool p/US09720934/runat 30062004_064540_13442/app_query.fasta_1.1386
-Q=(cgn2 1/USPTO_spool p/US09720934/runat 30062004_0 1_LOODECL=0 -LOODECL=0
-DEVENT=fastap -SUFFIX=rst -MINMATCH=0.1_LOODECL=0
-DISTALIGN=000-1-LIST=45
-DCCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=Ext -HEAPSIZE=500 -MINLENE 0 -MAXLENE=200000000
-USER=US09720934 @CGN 1 1 12421 @runat 30062004_064540_13442 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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303871 U 303871 U 960622 A 9729468 F738758 F738755 Q393010 W206547 W399663	BM466259 AGENCOURT CA886530 B0130E05- CC17874 XB484 Bay CC17874 XB484 Bay CA889924 B0156A01- BJ095151 BJ095151 B1155542 602903945 CB715459 AMGNNUC:M CA337260 UI-M-F70- AW761705 UQ22409.y CC200213 XG015 Bay CC8593264 AMGNNUC:C AV595297 AV595297 CF5539609 UI-M-GY0- BB656585 BB656585 BE792057 QV0-NN102 BX8799964 BR8799966		0 0 4 0 O	20063 DKFZp761L 340403 365659 M 643494 cm30d04. 90689 AV590689 911573 MR4-UT00	Description

ALIGNMENTS

REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AL120063	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteroscomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 527)	Homo sapiens (numan)	EST.	AL120063.1 GI:5925962	AL120063	DKFZp761L192 5', mRNA sequence.	DKFZp761L192_r1 761 (synonym: hamy2) Homo sapiens cuna cione	AL120063 527 bp mRNA linear EST 04-SEF-2003		

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                                                                                                                                                                 AUTHORS
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                                                                                                    Fahrenkrug.S.C., Smith,T.P.L., Freking,B.A., Cho, Vallet,J., Wise,T., Rohref,G.A., Pertea,G., Sultar Quackenbush,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 536)
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BI340403.1
 Contact: Smith TPL USDA, ARS, US Meat
                                                           22213789
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
                                       12226715
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Berlin- Charlottenburg, GERM
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone (DKFZp761L192) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (Contact: MIPS
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Unpublished (1999)
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                                                                      Genome
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/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
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/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="DKFZp761L192"
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   Animal
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Research Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 AATTTTAACAAAAATGATGTCATCACCGTCTTGGAGCAGCAGGACATGTGGTGGTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 GTGGAGGGGCTCCAAGCCCAAGCCCTGTATCCTTGGAGAGCCAAAAAGGACAACCATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                              Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, lyr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.

The NIEHS Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs

Gene 267 (1), 71-87 (2001)
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709
                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                    AW643494 Standard Source normalized Xenopus egg laevis cDNA clone PBX0129D04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                      AW643494.1
                                                                                                                                                                                                                                                                                                                                                                                                                            AW643494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4396
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 105 row: A column: 4 Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGTTCAAGGCCAGAAGGGTTGGTTCCCTAAGTCCTACGTGAAACTCATTTCAGGG
                                                                                                                                                                                                                                                       (bases 1 to 553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="MARC 2PIG"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: S
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 26-APR-2001
library Xenopus
                                                                                                                                                                                                                                Staffa, N.G
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RESULT 4
AV590689
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Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment
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                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Reser
Parkway, Huntsville, AL 35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
                                                                                                                                                                          294
                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                174 GTAGAAGGCCTTCAGGCACAAGCCTTGTATCCTTGGAGAGCAAAGAAGGACAACCATCTT
                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
AV590689 Bo:
5', mRNA sec
AV590689
AV590689.1
EST.
Bos taurus
                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                               1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: CAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: TGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR PRimers
                                                                                                     AV590689
                                                                                                                                                                                            GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly
                                                                                                                                                                                                                                                               AsnPheAsnLysAsnAspValIleThrValLeuGluGlnGlnAspMetTrpTrpPheGly
                                                                                                                                                                            GAAGTTCAAGGTCAAAAGGGCTGGTTTCCCAAATCCTATGTAAAGCTTATATCCCGGT
                                                                                                                                                                                                                                             AATTTTAACAAAAATGATGTTATCACGGTTCTTGAACAGCAGGATATGTGGTGGTTTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: T7 primer
   taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing and analyses th Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; PolyA-selected mRNA was prepared from unfertilized Xeno] laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Reseau 6:791-806, 1996. The first strand synthesis used a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6:791-806, 1996. The first strand synthesis used a NotI-dTIB primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 X 10.5
                                                                 sequence.
                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sue_type="unfertilized egg"
1_type="unfertilized egg"
__stage="unfertilized egg"
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                                                                                       brain
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Matches:
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Indels:
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                                                                                     EST 27-NOV-2001
ne E1BR014A10
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Best Local Similarity:
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                                                     REFERENCE
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                                                                                                      ORGANISM
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                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                         41 GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                     21 AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Establishment of a high throughput EST s poly(A) tail-removed cDNA libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                                                                                                                                                      MR4-UT0090-091100-002-e07
BF911573
BF911573.1 GI:12303031
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing.
This clone was obtained from a polyA-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos. 1 (bases 1 to 556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                        Homo
                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                 GAAGTTCAAGGCCAGAAGGGTTGGTTCCCCAAGTCCTACGTGAAACTCATTTCAGGG
                                                                                                                                                                                                                                                                                                                                                     AATTTTAACAAAAACGACGTCATCACCGTACTGGAGCAGCAAGACATGTGGTGGTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site 1: Sal1;
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="brain"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Bos taurus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="E1BR014A10"
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Gallus gallus
Gallus gallus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Gallus
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                                                                                                                             sequence.
BU272390
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.bk/scripts/gethtml2.pl?ti=MR4&t2=MR4-UT0090-
091100-002-e07&t3=2000-11.09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 40
High quality sequence start: 555.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudence 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
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Simpson, A.J.
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                                                                        gallus (chicken)
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/dev_stage="Adult"
/clone_lib="UT0090"
/clone_lib="UT0090"
/note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/site_2: SmaI; A mini-library was made by cloning products
derived from ORBSTES PGR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                          800 bp AGENCOURT 12983401 NICHD XGC Tad1 IMAGE:6877279 3', mRNA sequence.
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Xenopus laevis (African clawed frog)
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Department of Biomolecular Sciences
University of Manchester Institute
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/clone lib="CSEQCHN52"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
/clone progan: limbs; Vector: pBluescript II KS(+); Site_1:
/clone progan: limbs; Vector: pBluescript II KS(+); Site_1:
/constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
/collowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
/coordinatible sites of a custom modified MCS of the
/compatible sites of a custom modified MCS of the
/counds using conditions adapted from Soares et al., PNAS
/(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
/(1996): 791, except that a significantly longer
//clone program of the part                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01612008930
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                                                                                                                                   AGENCOURT 12983387 NICHD XGC Tad1
IMAGE:6877279 3', mRNA sequence.
CB756047
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Sequenced with vector primer
Tissue Procurement: Drs. Donald Brown and Liquan
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                         Xenopus laevis (African clawed frog)
Xenopus laevis
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/dev stage="metamorphosis stage 53"
/clone_lib="NICHD_XGC_Tadl"
/clone_lib="NICHD_XGC_Tadl"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
/note="Organ: DNR-LIB;
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/mol_type="mRNA"
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US-09-720-934-2_COPY_908_966 (1-59) x CB756047 (1-847)
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                                                                                                                                            CF172865 S97 bp mRNA linear B0915A02-5 NIA Mouse Unfertilized Egg cDNA Library musculus cDNA clone NIA:B0915A02 IMAGE:30473665 5', CF172865
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Sequenced with anchor primer
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 847)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                 Mus musculus
                                                                                                                       CF172865.1
                                                                        Mus musculus (house mouse)
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Location/Qualifiers
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/clone lib="NICHD_XGC_Tad1"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used i
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCGACATG-dT(3)BN-3' (where B = A,
C, G, or T). Average insert size 1.6
(range 0.9-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones an
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Plate: B0915 row: A column: 02
Seq primer: M13 Reverse
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to Piao, Y., Ko, N.
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                                              AATTTTAACAAAAGTGACGTCA†CACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGA
                                                                             AsnPheAsnLysAsnAspVall1eThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
GluValGinGlyGlnLysGlyT†pPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 597)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Bal4, purified by penenol/chloroform, and separated from tree linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH1DB E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was
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5'-paacragroupaarcacaagcagcacccrrrrrrrrrrrrrr-3'],
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/dev_stage="Unfbrtilized Egg"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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Db 472 GAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGG 528

CP174208 606 bp mRNA linear EST 25-JUL-2003 B0935F02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0935F02 IMAGE:30475645 5', mRNA sequence. 1 (bases 1 to 606)
Piao, Y., KO, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification Email: cdna@lgsun.grc.nia.nih.gov Plate: B0935 row: F column: 02 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Seq primer: M13 Reverse Contact: Dawood B. Dudekula 21429098 Genome Res. 11 (9), 1553-1558 (2001) method Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mus musculus Mus musculus (house mouse) CF174208.1 CF174208 Laboratory of Genetics treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was quality sequence stop: 606 Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544193]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) Site_2: NotI; Mouse cDNA project by the Laboratory of constructed /mol_type="mRNA" /strain="C57BL/6J" Location/Qualifiers note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; /dev_stage="Unfertilized /lab_host="DH10B" clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long clone="NIA:B0935F02 IMAGE:30475645" /db_xref="taxon:10090" db_xref="niaEST:B0935F02-5" organism="Mus musculus" GI:33283757 by Yulan Piao

3.62e-35 323.00 100.00%

Conservative:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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IMAGE:5695975 5', mRNA sequence.
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BM944544.1
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National Institutes of Health, Mammalian
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          /dev stage="embryo 18.5 dpc"
/lab host="DH10B (T1 phage resistant)"
/clome lib="NIH_BMAP_EHOp"
/clome lib="NIH_BMAP_EHOp"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Grgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library kag
sequence located between the Not I site and the polyA
tail, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone was contributed by the Brain Molecular Anatomy Project
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/strain="C57BL/6"
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us musculus cDNA clone
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                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.L., Feingold, E.A., Grouse, I.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, E. D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527
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Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                     Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC062938 5385 bp mRNA linear HTC 11-DEC-200: Mus musculus intersectin (SH3 domain protein 1A), mRNA (cDNA clone IMAGE:6839463), containing frame-shift errors.
                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                        Strausberg, R.
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                   Single pass sequencing. trimmed with the aid of cross match v0.990329.
                                                                                                                                                                               Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
Contact: Rexroad CE
                                                                                                                                                                                                                                                                                                                                                                                                                              CA360651
634174 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT108K03_A_F02
5', mRNA sequence.
                                  Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with
trimmed with the aid of the trim_alt optic
                                                                                                                                                                                                                                        Protacanthopterygii; Salmoniformes; Salmonidae; 1 (bases 1 to 434)
Rexroad, C.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC blone distribution informati
through the I.M.A.G.E. Cbnsortium/LLNL at: http://in
Series: Plate: Row: Cblumn: 0
This clone has the following problem: frame shifted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: bento-soares@uibwa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                      Tel: 304 724 8340 x2129 Fax: 304 725 0351
                                                                                                                                          USDA, ARS, National Center for Cool
11876 Leetown Road, Kearheysville,
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                               Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                      Oncorhynchus mykiss (raipbow trout)
                                                                                                                                                                                                                                                                                                                                                                                                               CA360651.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluValGlnGlyGlnLysGlyTkpPheProLysSerTyrValLysLeuIleSerGly
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  primer:
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/tissue_type="Brain"
/clone_lib="NIH_BMAP_GH0"
/lab_host="DH10B"
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/strain="C57BL/6"
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                                      red v0.020425.c and
Vector identified
                                                                                                                                                                                                                                                                                       Oncorhynchus.
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                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뮹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GTGGAGGGTTTGCAGGCTCAGGCTCTGTACCCGTGGCGGCCAAGAAGGACAACCACCTC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ179493 690 bp mRNA
UI-M-EWO-bww-k-03-0-UI.r1 NIH_BMAP_EWO 1
IMAGE:5704058 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ179493.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ179493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGTGCAGGGCCAGCGGGCTGGTTCCCCAAGTCCTACGTCAAGCTCATCTCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTTCAACAAGAGCGACGTGATCACAGTGCTGGAGCAGCAGGACATGTGGTGGTTCGGC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnPheAsnLysAsnAspVallleThrValleuGluGlnGlnAspMetTrpTrpPheGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 690)
                                                                                                                                                                                       primer: pYX-5
                                                                                                                                                                                                                                clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db xref="reaxon:8022"
/clone="1RT108K03 A F02"
/tissue_type="pooled"
/lab host="PH10B"
/lab host="PH10B"
/clone_lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."
/clone="IMAGE:5704058"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                              /db_xref="taxon:10090"
                                                                                                                                                                      Location/Qualifiers
                                                                                 strain="C57BL/6"
                                                                                                     mol_type="mRNA"
                                                                                                                        organism="Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.98e-35
320.00
100.00%
96.61%
97.56%
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                                                                                                                                                  .690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (house mouse)
                                                                                                                             musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x CA360651 (1-434)
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 30-APR-2002
cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
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US-09-720-934-2_COPY_908_966 (1-59) x BQ179493 (1-690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 uAsnPheAsnLysAsnAspValIleThrValLeuGluGlnGlnAspMetTrpTrpPheGl 40
                                                                                                                                                                                                                                                                              CB435046 694 bp mRNA linear 611770 MARC 6BOV Bos taurus cDNA 5', mRNA sequence. CB435046 CB435046.1 GI:29215685 EST.
Bos taurus (COW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲
                                                                                                                                                                          cross_match v0.990329.

Plate: FQY8036 row: O column: 9
Seq primer: GTAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A second set of bovine ESTs from pooled-tissue Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yGluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 694)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EW0"
/note="Organ: brain; 'Vector: pYX-Asc; Site_1: EcoR I;
/
/organism="Bos taurus"
/mol_type="mRNA"
                                                                                                                                  Location/Qualifiers
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310.00
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 25-MAR-2003
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DEFINITION ACCESSION VERSION

RESULT 15 CB435046

LOCUS

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KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

COMMENT

TITLE JOURNAL

FEATURES

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                                                                                                                                                                                     US-09-720-934-2_COPY_908_966 (1-59)
                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                         Pred
                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                         No.:
240 AGAAGTTCAAGGCCAGAAGGGTTGGTTCCCCAAGTCCTACGTGAAACTCATTTCAGGG
                                                              180 AATGTGGAACAAAAACGACGTCATCACCGTACTGGAGCAGCAAGACATGTGGTGGTTTTGG
                                                                                                                          Similarity:
                  40 yGluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly
                                                                                  21 Asn-PheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGl
                                                                                                                                                       1 ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
                                                                                                                                                                                                                                                                                                                                                                    /note="Tvector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="MARC 6BOV"
/note="Vector: pcDNA3...
                                                                                                                                                                                                                        3.03e-33
310.00
98.33%
96.67%
94.51%
                                                                                                                                                                                          x CB435046 (1-694)
                                                                                                                                                                                                                                      Conservative: Mismatches: Indels:
                                                                                                                                                                                                                        Gaps:
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297
                              59
                                                               239
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                                                                                                                                                          20
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ORIGIN

. No.:

Search completed: July 1, 2004, 19:48:48 Job time: 1780.84 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09720934/runat_30062004_064539_13430/app_query.fasta_1.1386
-DB-GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 -END=-1 -THRAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -CORE=pct -THRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USEX=US09720934 @CGN 1_1 7509 @runat 30062004 064539 13430 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
DB
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seq length: 2000000000
9: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Leukemia and utilization thereof
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Leukemis SINAI HEALTH SYSTEM ET AL
OS Homo sapiens (human)
PN p 2002511267-A/5
PN p 2002511267-A/5
PD 16-APR-2002
PD 16-APR-1999 UP 2000543610
PR 16-APR-1998 US 60/082007
PR 16-APR-1998 US 60/082007
PI JULIE R KORENBERG, XLAO NING CHEN
C12015/9, A01X67/027, C07X14/47, C07X16/18, C07X19/00, C12N15/10,
PC C1201/68, C01X33/68/A61X48/0b, C12N15/00, C12N5/00
CC Isolated SH3 gene relating to myeloproliferative disorders ar
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3231)
Korenberg, J.R. and Chen, X.N.
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Isolated SH3 gene relating to myeloproliferative disorders and
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C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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                 GI:1438932
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                            domain-containing protein SH3P17
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complete cds.
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AF132672.1 G
                                                         AF132672 3812 bp mRNF
Rattus norvegicus EH-domain/SH3-domain
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Nat. Biotechnol. 14 (6), 741-744 (1996)
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1 (Dases 1 to 3241)
Sparks, A.B., Hoffman, N.G., McConnell, S.J., Fowlkes, D.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (18-JUN-1996) CYTOGEN Corp.,
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SYVKLISGP1RKSTSWDSGSSSSPASLKRVASPAKKFVVSGEELAQVIASYTATGPEQ
KITLAPGQLILIKKKNPGGMWEGELQARGKKRQIGWFPANYVKLLSPGTSKSTTPTEPSK
STALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLFPSNY
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/protein_id="AAC50592.1"
/db_xref="GI:1438933"
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                                           3041 GGAGAAGAATCGCCCAGGTCATTGCTTCCTACACTGCTACGGGTCCTGAACAGCTCACC
                                                                        21 LeuAlaProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGly
                                                                                                                                                                    1 GlyGluGluIleAlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-MAR-1999) Center for Basic Neuroscience and HHMI, Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHSH1/intersectin, a protein that contains EH and SH3 domains and binds to dynamin and SNAP-25. A protein connection between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75235, USA
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GluLeuGlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLys 60
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NRRQELLTQRNKDQEGT VULKARKKTLEFELBALDKKKHQLEGEUQDI RCILATORQE
IESTINKSELB LAEI THLQQQLGESQONLGRIL PEKQI LSDQLKQVQQUSLHRDSLT
LKRALEAKELARQLREQLDEVEKSTRSKLQEIDVENNQLKEIRE IHSKQQLQKORSI
EARRLKQKEGARQLEEQKKEGGRRSKLQEIDVENNQLKEIRE HSKQQLQKORSI
EARRLKQKEGARVSLELEKQKEEGQRRVQEEDQRPRKPHEEDKLKR
EDSVXKKEAERERAKPBYODKOGSLFHEHHQEBAKRAQARAWFTEKGPLTISAGNSAKVY
YYRALYPFESRSHDEITIQPGDIVMVKGEWVDESQTGEPGMLGGEPKGKTGWFPANYA
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STNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQ
AQALYPWRAKKDNHLNFNKSDVITVLEQQDWWWFGEVQGQKGWFPKSYVKLISGPVRK
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KQQPAAISSAPAFGIGGMAGMPPLTAVAPVPMGSIPVVGMSPPLVSSVPQAAVPPLAN
GAPPVIQPLPAFAHPAATLPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPAAAEWAVP
QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
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SEDEQQVEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQER
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/protein_id="AAD31026.1"
/db_xref="GI:4838526"
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/mol_type="mRNA"
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3161 GAACTACAAGCTCGAGGGAAAAAGCGCCAGGATAGGGTGCTCCCAGCAAATTATGTCAAA 3220
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
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Direct Submitssion
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone (DKFZp686J17173) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14055 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research (enter (DKrZ); kmall s.wlemann@dktz-neldelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
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Fobo, G., Han, M. and Wiemann, S.
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/clone_Tib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
pH10B; sites SfiIA + SfiIB"
                                                                                                                                                                                                                                                                       PGSQLNTKLQKAQSFDVASVPPVAEWAVPQSSRLKYROLFNSHDKTMSGHLTGPQART
ILMGSSLPQAQLASI WNLSDLDQDGKLTABEET LAMHLI DVANSGQPLPPVLPPBYI P
BSPRRVRSGSGISVI SSTSTVDQRLFBEPVLEBDEQQLEKKLPVTFEDKKRENERGHL
ELEKERQALLEQQRKEQERLAQLERAEQERKERERGBGBKKQLELEKQLEKQLEKQRELER
GREEERKE I ERREAAKRELERQROLEWERNRRGELLNGRNKEGED I VVLKAKKKTLE
FELEALNDKKHQLBGKLQDI RCLTTTQRQEI ESTNKSREELR I AEITHLOQLOGSOQL
GRALI PEKQI LNDQLKQVQQNSLHRDSLVTLKRALEAKELARQHLRDQLDEVEKETRS
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QERDKQWLEHVQQEDEHQRPRKLHEEEKLKREESVKKKDGEEKGKQEAQDKLGRLFHQ
HQEPAKPAVQAPWSTAEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMV
                                    /gene="DKFZp686J17173"
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/gene="DKFZp686J17173"
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/protein_id="CAD98050.1"
/db_xref="GI:31874621"
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/map="21q22.11"
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Korenberg, J.R. and Chen, X.N.
Isolated SH3 gene relating to myeloproliferative disorders leukemia and utilization thereof Patent: JP 2002511267-A 1 16-APR-2002;
CEDARS SINAI HEALTH SYSTEM ET AL
OS Homo sapiens (human)
PN JP 2002511267-A/1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Isolated SH3 gene relating to myeloproliferative disorders
leukemia and utilization thereof.
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Isolated SH3 gene relating to myeloproliferative disorders and
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16-APR-1998 US 60/082007
JULIE R KORENBERG, XIAO NING CHEN
C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon: 9606"
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    1.16e-32
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99303609
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Okamoto,M., Schoch,S. and Sudhof,T.C.
EHSH1/intersectin, a protein that contains
binds to dynamin and SNAP-25. A protein con
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J. Biol. Chem. 274 (26), 18446-18454 (1999)
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Mammalia; Eutheria;
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NRRQELLTQRNKÖQEGIVÜLKARRKTLEFELEALNDKKHQLEGKLQDIRCKLATORQE
IESTNKSRELRIABITHLQQQUQESQQMLGRLIPEKQILSDQLKCVQQQNSLHRDSLLI
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EAERLLAKELARQQLAEQLDEVEKFRSKLQSIDVENNOLKELLEIHSKOQLOKOKSI
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EDSVKKKEAEERAKPEVQDKGSRLFHHQEPAKPAQAFWFTTEKGPLTISAQESAKVV
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EKIPENEIPTPAKPVTDLTSAPAPKLALRETFAPLFVTSSEPSTTENNWADFSSTWPS
                                                                                                                                                                       EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSYIPSGSGMSVISSSSADQRLPEEPS
SEDEQQVEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQER
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                                                                                                                                                                                                                                                                                                                                                             /product="EH- and SH3-domain containing
/protein_id="AAD30271.1"
/db_xref="G1:4835853"
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/mol_type="mRNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                               CEDARS SINAI HEALTH SYSTEM ET AL

OS Homo sapiens (human)

PN JP 2002511267-A/3

PD 16-APR-2002

PF 16-APR-1999 JP 2000543610

PR 16-APR-1998 US 60/082007

PI JULIE R KORENBERG, XIAO NING CP

CC 22815/09, A01K67/027, C07K14/47

PC C129168,
PC G01N33/68//A61K48/00, C12815/00

CC Isolated SH3 gene relating to
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Korenberg, J.R. and Chen, X.N.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JP 2002511267-A/3.
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16-APR-1999 JP 2000543610
16-APR-1998 US 60/082007
JULIE R KORENBERG, XIAO NING CHEN
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                                                                                                                                                         utilization thereof.
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                          Location/Qualifiers
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KDGDWWTGTVGETSGVFPSNYVRLKDSEGSGTAGKTGSLEKKPEIAQVIASYTATGPE
QLTLAPGQLILIRKKNPGGWNEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELP
KTAVQPAVCQVIGMXDYTAQNDDELAFSKGQIINVLSKEDPDWWKGEVSGQVGLFPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5381)
                                                                                                                                                                                                                                                                                                                                                             Cancer Research Institute, L'Hospitalet de Llo.,
Castelldefels km. 2,7, Barcelona 08907, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 5381)
Pucharcos, C., Fuente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99415290
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGTCAGCTGATTTTGATCCGAAAAAAGAACCCAGGTGGATGGTGGGAAGGAGGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3637
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/codon_start=1
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/product="intersectin short isoform"
/proteain_id="AnD29953.1"
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GAPPVIQPLPAFAHPAATLFKSSSFERSGPGSQLNTTKLQKAGSFDVASVPPVAEWAVP
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTP
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269. .3931
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/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                    'gene="ITSN"
                                                                                                                                                                                                                                            /map="21q22.1-q22.2"
                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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RESULT 9
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Isolated SH3 gene relating to myeloproliferative disorders and leukemia and utilization thereof
Leukemia and utilization thereof
Leukemia solutilization thereof
CEDARS SINAI HEALTH SYSTEM ET AL
LOS Homo sapiens (human)
PN JP 2002511267-A/2
PD 16-APR-1999 JP 2000543610
PR 16-APR-1998 US 60/082007
PI 16-APR-1998 US 60/082007
PI 16-APR-1998 US 60/082007
PI JULIE R KORENHERG, MIAO NING CHEN
PC C12015/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
PC G01N33/68/JAG1K48/00,C12N15/00,C12N5/00
CC Isolated SH3 gene relating to myeloproliferative disorders an
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Korenberg, J.R. and Chen, X.N.
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BD205034.1 GI:33014804
JP 2002511267-A/2.
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                                                                 16-APR-2002

16-APR-1999 JP 2000543610

16-APR-1998 US 60/082007

JULIE R KORENBERG, XIAO NING CHEN

C12N15/09, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
  G01N33/68//A61K48/00,C12N15/00,C12N5/00 Isolated SH3 gene relating to myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5458 bp DNA linear PAT 17-JUL-2003 SH3 gene relating to myeloproliferative disorders and and utilization thereof.
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GPEKSTALAAVCQVLEWYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF
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NYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTPNNWADFSST
WPTSTNEKPETDNWDAWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSFVLGQGEKVE
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TLKRALEAKRILARDILRODLDEVEKTRSKLGEDITRNOLKELREIHKKQLAQKSK
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rkererqeqerkrqlelekqlekqrelerqreberrke1erreaakkelerqrqlewe
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Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Bur. J. Hum. Genet. 7 (6), 704-712 (1999)
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                                                                                                                                  Cancer Research Institute, L'Hospitalet de Llo., Avia. Castelldefels km. 2,7, Barcelona 08907, Spain
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Pucharcos, C., Fuente
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Mammalia; Eutheria;
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                                                /organism="Homo sapiens"
/mol_type="mRNA"
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                 /chromosome="21"
/map="21q22.1-q22.2"
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TLKRALEAKELARQHLRDQLDEVEKETRSKLQEID I FNNQLKELÆIHNKQLQKQKS
MEARRLKOKEGORK I ELEKGKEBAGRRAGERDKOWLEHVOGEDBHORFRKLHEESKL
KRESSVEKKNOESEKGKOEADORLGRLIFHGOLDER KREAVQADPMSTJAEKGELTISAQENV
KVVYYRALYPPESRSHDEITIQPEDI VMVKGEMVDESQTGEPGMIGGELKGKTGWFBA
NYAEKLIPENEVAPVENTDSTSAPAPKLALRETPAPLAVTSSEPSTTENNWADESST
MPTSTNEKFETDNWDAMAAGPSLTVESAFQLROKGAFTPATATGSS PSPVLGQGEKVE
GLQAQALYPMRAKKDNILNFNKNDVITVLEQDDMWWFGEVQGQKGWFPKSTVKLISGP
IRKSTSMDSGSSESPASIKRVASPAREVVSGEEFIAWTTESSERGELTSSYTÄT
GPEQLTLAPGQLILIRKKNPGGEMWEGELQARGKKRQIGWFPANYVKLLSPOTSKITFI
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PSNYVKLTTOMDPSOQMCSDLHLLDMLTFTETEKRGVIHELIVTEENVNDLOLVTEI
FQKPLMRSELLITEKEVAMIFVNMKELIMCNIKLLKALKVEKKMSGEKMPVKMIGDILS
AOLPHNOPYIRPCSROLNGAALLOOKTDEAPDFKEFVKAMADERCKGWPLSSFILKP
AOLPHNOPYIRPCSROLNGAALLOOKTDEAPDFKEFVKAMADERCKGWPLSSFILKP
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QAHVQCEGLSBQLVFNSVTNCLGPRKFLHSGKLYKAKSNKELVGPLFNDFLLITQITK
PLGSSGTDKVFSPKSNLYQKMYKTPIFLNEVLKLPTDPSGDEPIFHISHIDRVYTLR
AESINBRTAWYQKIKAASELYIETEKKKREKAYLVRSQRATGIGRLMVNVUGGIEIKK
QRSINBRTAWYQKIKAASELYIETEKKKREKAYLVRSQRATGIGRLMVNVUGGIEIKD
CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKMNSNCQPFIRDLEQEVLCITVFERDQ
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsyba,L.O., Kvasha,S.M Slavov,D., Tassone,F., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1996)
Tsyba, I.O., Kvasha, S.M., Skripkina, I.Y., Anoprienko, O.V.,
Slavov, D., Tassone, F., Ryndirch, A.V. and Gardiner, K.
Mouse homologs of human chromosome 21 genes
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                                               AF064243.1
                                                                                             AF064243
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                                                                                                                                                                  CTTCTAAGCCCT 317
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sapiens
sapiens
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/tissue_type="brain"
/dev_stage="infant"
<1. .1996</pre>
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IAQVIASYTAAGPEQLTLAPGQLILIRKKNPRGWWEGELQARGKKRQIGWFPANYVKL
LSPGTSKITPTEPPKSTALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGEVNGQVGLFPSNYVKLTTDMDPSQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
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/db_xref="taxon:9606"
/chromosome="21"
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Tassone,F., Rynditch,A.V. and
              (human)
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  Percent Similarity:
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1 (bases 1 to 5287)
Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michel-Servet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antonarakis,S.E.
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KVYYYKALYPPESRSHDEITIQPGDIVWVKGEWTDESOTGEPGWLGGELKGKTGWFPA
NYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTUMWADFSST
WPTSTWEKPETDWWDAWAAQPSLTVPSAGQLKQRSAFTPATATGSSPSPEVLGGEKVE
GLQAQALYPWRAKKDWHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGP
GLQAQALYPWRAKKDWHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGP
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GLQAQALYPWRAKKDWHLNFNKNDVITVLEQCDMWWFGEVGGOKGWFYKSYVKLISGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC78610.1"
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RQQPVAISSAPPFGMGGIASMPPLTAVAPVPMGSIPVVGMSFILVSSVPTAAVPPLAN
KQQPVAISSAPPFGMGGIASMPPLTAVAPVPMGSIPVAGQSFDVASVPVABAVP
GAPPVIQPLPAFAHPHATLTPKSSSERSGFGGOLWTKLQKAQSFDVASVPVABAVP
GSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
                                                                                                                                                                                                                                                                                                         /note="encodes 3110. .3286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYYKLLNPGTSKITPT
EPPKSTALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNRRQELLNQRNKEQEDI VVLKAKKKTLEFELEALNDKKHQLEGKLQDI RCRLTTORQ
EI ESTNKSREUR I AEI THLQQLQESQQMLGRLI FENGLIKQVQQNSLHROSLV
TLKAALEAKELARGHLROQLDEVEKGTRSKLQBIDI FENGLKELERI HIKKQLQOKOS
MEAERLKQKEQERKI LELEKQKEEAQRRAQERDKQMLEHVQQEDEHQR PRKLHEEEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPV
LEDEQQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQE
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M., Scott,H.S.,
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product="intersectin short
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|mol_type="mRNA|"
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Antonarakis, S.E.
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Two isoforms of a human intersectin (ITSN) protein are produced by brain-specific alternative splicing in a stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF064244.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluIleAlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerPro 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCACGTGGGAAAAAGCGCCAGATAGGCTGGTTCCCAGCTAATTATGTAAAGCTTCTA
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                                                                                                                                               /codon_start=1
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                       LEDEQQOLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEGERLAQLERAEGE RKERERGEGEKKRQLELEKGRLEEGEKGNLEWE RKERERGEGEKKGLEKGRLEEGEKGLEWE RNRRGELLNGRNKEGEDI VVLKAKKKTLEFELEALNDKKHOLEGKLGDI LECRLITTGRQ EIESTINKSRELRIAEITHLQQQLGESQQMLGRLIPEKGILNDQLKQVQQNSLHRDSLV TLKRALEAKELARGHLRDQLDEVEKETRSKLGEIDI TENNQLKELRE IHNKQQLGXGKS MEAERLKÇKEGEKLT IELEKQKEBAQRRAQERDKQMLGHVQQEDEHQRPRKLHEEEKL
                                                                                                                                                                                                                                                                                                                                                                                       107
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KREESVKKKDGEEKGKQEAQDKLGRLFHQHQEPAKPAVQAPWSTAEKGPLTISAQENV
                                                                                                                                                                                                                                                                                                                                                                                                                               /map="21q22.1-q22.2"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                        dev_stage="fetus"
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Mus musculus Esel protein
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EPPKSTPALAAVCQVIGWYDYTAQNDDELAFNKGOI INVLNKEDPDWWKGEVNGQVGLF
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AESINERTAWVQKIKAASELYIETEKKKEEKAYLVRSQRATGIGRLMVNVVEGIELKE
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CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKMNSNCQFFIEDLEGVLCITVFERDQ
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GLQAQALYPWRAKKDNHLNENKNDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLLSGP
IRKSTSMDSGSSESPASLKRVASPAAKPVVSGEEFIAMYTYBSSEQGDLTATGQGBVTL
VTKKDGWWTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYTAT
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NYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTPNNWADFSST
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4649. .4819
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3569. .3748
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 3723)
Sengar,A.S., Wang,W., Bishay,J., Cohen,S. and Egan,S.
                                                                              Mus musculus
                                                                                                                                              Mus musculus Esel protein
AF132478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-JUL-1999) Department of Molecular Oncogenetics, Institute of Molecular Biology and Genetics of National Academy of Sciences of Ukraine, 150, Zabolotnogo str., Kiev 252627, Ukraine Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsyba,L.O., Kvasha,S.M., Skripkina,I.Y., Anoprienko,O.V., Slavov,D., Tassone,F., Rynditch,A.V. and Gardiner,K. Mouse homologues of human chromosome 21 genes
                                                                                            Mus musculus
                                                                                                                               AF132478.1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EQGDLTFQQGDVIVVTKKDGDMWTGTVGDKsGVFPSNVVRLKDSEGSGTAKTGSIGK
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VKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDP
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/product="Ese1 protein"
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/db_xref="taxon:10090"
/dev_stage="15~day embryo"
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Indels:
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Best Local Similarity:
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99164083
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Research/Developmental Biology, The Hospital for Sick Children, 555
University Avenue, Toronto, ON M5G-1XB, Canada
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Direct Submission
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EEFILAMHLIDVAMSGQPLPPVLPPBY I PPSERRVRSGSGMSVISSSVDQRLPBEPS
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YPWRAKKDMHLNENKSDVITTLEGQDWMWFGEVQGGKGWFFKSTYKLISGPVRKSTSI
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WWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIAS YAATGPEQLTL
APGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELFKTAV
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2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-475-894-3

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US-08-474-709-1

US-08-484-710-1

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equence 29,	quence 1	equence 1,	equence 28,	equence 30,	equence 11,	equence 25,	equence 1,	equence 68,	equence 3,	equence 187	equence 120	equence 12	equence 9,	quence 12:	equence 12	equence 3,	equence 3,	equence 1,	equence 1,	equence 39"	equence 5,	equence 5,	equence 5,	equence 5,	equence 15!	equence 3,	equence 1,	equence 3,	equence 19	equence 13!	quence 1	equence 79, App

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ALIGNMENTS

RESULT 1

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US-08-630-915A-39
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APPLICANT: SPARKS,
APPLICANT: HOFFMAN,
APPLICANT: KAY, Bri
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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STREET: 115
                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1155 Avenue
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                    1101-174
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(212) 869-8864/9741

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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                COUNTRY: USA
ZIP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/63D,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NUMBER: US/08/63D,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
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STATE: New Yor
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STRANDEDNESS: single
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STREET: 1155 Avenue of the
TELEPHONE:
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o. 6309820
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                                                                  Misrock, S. Leslie
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VENTION: POLYPEPTIDES HAVING A FUNCTIONAL

VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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1, No. 630982Dh
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DB:
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Best Local Similarity:
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     TELEFAX: (617)44
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
mucleic acid
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                                                                             NAME: Louis Myers

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
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                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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NAME: Louis Myers
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MEDIUM TYPE: Floppy disk
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 LENGTH: LUCIEIC F
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CLASSIFICATION:
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STRANDEDNESS: single
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STRANDEDNESS:
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; TOPOLOGY:
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US-08-475-894-3
Score:
             Alignment Scores:
Pred. No.:
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Best Local Similarity:
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APPLICANT: Yen-Mi
                                                                                                                                                                          TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                               MOLECULE TYPE:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BG:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
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                                                                                                          STRANDEDNESS:
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                                                                                              TOPOLOGY:
                                                                                                                               TYPE:
                                                                                                                                                                                                                                                          NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/484,710
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                                                                                                                        nucleic acid
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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DB:
US-09-720-934-2_COPY_999_1062 (1-64) x US-08-484-709-3 (1-1392)
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Best Local Similarity:
                                                                                                                                                                       US-08-484-709-3
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                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
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CITY: Boston
STATE: Massac
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REGISTRATION NUMBER: 35.
REFERENCE/DOCKET NUMBER:
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TOPOLOGY: lir
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SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Louis Myers
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ADDRESSEE: LAHIVE & COCKFIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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MEDIUM TYPE: Floppy disk
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US-08-484-710-1
                                             US-08-484-709-1
                                                            RESULT
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               Sequence 1, Application US/08484709 Patent No. 5837844
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Sequence 1, App...
GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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VENTION: THE CAIP-LIKE GENE FAMILY
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                                                                                                                                Sequence 1, Application Patent No. 6171800
                                                                                                                GENERAL INFORMATION:
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NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                APPLICANT: Yen-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ADDRESSEE: LAHIVE & COCKFIELD
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TOPOLOGY: lir
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CLASSIFICATION:
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INVENTION:
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                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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LENGTH: 1659 base pairs
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                         APPLICANT: Hau, Ye.
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                                                                                                    STREET: STREET:
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OPERATING SYSTEM:
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                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                            Patent No.
                                                                                                                                                          Sequence 48, Application US/08306691B
                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/475,710
FILING DATE: 07-UAN-1995
APPLICATION NUMBER: US 08/474,697
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                TITLE OF INVENTION: AN TITLE OF INVENTION: OL NUMBER OF SEQUENCES: 5
                                                                               APPLICANT: Calabrett
APPLICANT: Skorski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/484,709 FILING DATE: 07-JUN-1995
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                      1342
                                                                                                                                                                                                                                  1387 AAGTTACTTCCACCG 1401
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                                                                                                                                                                                                                                                                   60 LysLeuLeuSerPro 64
                                                                                                                                                                                                                                                                                                                                        40 GlyGluLeuGlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrVal 59
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                                                                                                                                            573403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                       Calabretta, Bruno
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Seidel, Gonda, Lavorgna & Monaco, P.C.
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Matches:
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STREET: Two Penn Center, Suite 1800 CITY: Philadelphia

Pennsylvania : U.S.A.

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RESULT 13
PCT-US93-06251-79
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-720-934-2_COPY_999_1062 (1-64) x US-08-306-691B-48 (1-2757)
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                                                                                                                                                                                            Sequence 79, Application PC/TUS9306251
GENERAL INFRAMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                COUNTRY: U
ZIP: 11530
                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 568-5549
                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                      2451 ---GTTGGCTGGTTCCCTGCCAACTACGTGGAG 2480
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                                                                                                                    Garden City
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                                                                                                                                    E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                  USA
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IBM PS/2
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111.00
58.82%
41.18%
32.55%
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RESULT 14
US-07-646-537B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07646537B Patent No. 5348864
          APPLICATION NUMBER: US/07/646
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER:
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CITY: Princeton
                                                                                                                                                                                                                                                                COUNTRY:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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TYPE: nucleic acid
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                                                                                                                                                                                                                                            08543-4000
                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                        P.O. Box 4000
                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Barbacid, Mariano
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111.00
58.82%
41.18%
32.55%
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                                                                                                          US/07/646,537B
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TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: TYPE: n

2793 base pairs

TYPE: nucleic acid STRANDEDNESS: double

TELECOMMUNICATION INFORMATION:

(609) 921-5901

TELEPHONE:

TOPOLOGY: linea MOLECULE TYPE: cI HYPOTHETICAL: NO

linear

cDNA

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US-09-023-655-1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1356, Application US/09023655 Patent No. 6607879
             APPLICATION NUMBER: US/09/028
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESSE: INCYTE PHARMACEUT CALS,
ADDRESSEE: 1174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jeffrey J. Seilhamet
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhame
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2495 --- ATCGGCTGGTTCCCTTCTAACTATGTGGAG 2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2387 TTCTGTGCCCGGGACAGGTCGGAACTGTCCCTTAAGGAGGGTGATATCATCAAGATCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 ArgLysLysAsnProGlyGlyTtpTrpGluGlyGluLeuGlnAlaArgGlyLysLysArg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 TyrThrAlaThrGlyProGluGlnLeuThrLeuAlaProGlyGlnLeuIle---LeuIle
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PA-0001 US
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Matches:
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Indels:
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US-09-023-655-1356
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GENBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                   432 GCTTATGTGAAATTTAACTACATGGCTGAGAGAGGAGGATGAATTATCATTGATAAAGGGG 491
                                                                 492 ACAAAGGTGATCGTCATGGAGAAATGCAGTGATGGGTGGTGGCGTGGTAGCTACAATGGA 551
                       45 ArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrVal 59
                                                                                                25 GlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeuGlnAla 44
                                                                                                                                                                  5 AlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAlaProGly
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36.36%
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CAAGTTGGATGGTTCCCTTCAAACTATGTA
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Matches:
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24

Search completed: July Job time: 49.815 secs 1, 2004, 19:53:56

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Command line parameters:

MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09720934/runat_30062004_064541_13481/app_query.fasta_1.1386
-DB=Published_Applications_NA_-QFMT=fastap_-SUFFIX=rupb_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US09720934_@CGN_1_1500_@runat_3062004_064541_13481
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - nucleic search, using frame_plus_p2n model
                                             and is
                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq
                                             derived
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length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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(cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                             analysis
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_6/ptodata/1/pubpna/US08_<u>PUBCOMB</u>.seq:*
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SUMMARIES
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ALIGNMENTS

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RESULT 1
US-10-564-049-887
Sequence 887, Application US/10264049
Publication No. US/20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION UNUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
FRIOR APPLICATION NUMBER: US 60/209,467
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
VMMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 887
LENGTH: 2067
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
LOCATION: (5)...(5)
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Result No.

Score

Query Match Length DB

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Description

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US-09-879-957-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (2063)...(2063)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (2058)..(2058)
OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
The Amer:
                             APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-D05/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                    APPLICATION NUMBER: US/09/879,957
ETILING DATE: 13-Jun-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPFIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 ProGlyGlnLeuIleAeuIleAkgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AAATTGCCCCAGGTTATTGCCTCATACACCGCCACCGGCCCCGAGCAGCTCACTCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GluīleAlaGlņValīleAlaSþrTyrThrAlaThrGlyProGluGlnLeuThrLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGCACGTGGGAAAAAGCGCC
                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGTCAGCTGATTTTGATCCGAAAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAGCTG 181
REGISTRATION NUMBER: 18,872
                NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                 TRY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPARKS, Andrew B. HOFFMAN, No. US20020034755A1h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAY, Brian K.
FOWLKES, Dana M.
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95.16%
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Matches:
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Indels:
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US-09-879-957-193
, Sequence 193, Application US/09879957
, Patent No. US20020034755A1
, GENERAL INFORMATION:
, APPLICANT: SPARKS, Andrew B.
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DB:
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Best Local Similarity:
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             ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: Pennie
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer
                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                        CITY: New York
APPLICATION NUMBER: US 08/630,915
                                                                                                                                                                                                                                                                                                                                                        McCONNELL, Stephen J.
OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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STRANDEDNESS: single
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HOFFMAN, No. US20020034755Alh
KAY, Brian K.
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                                Best Local Similarity:
Query Match:
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US-09-764-875-176
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DB:
US-09-720-934-2_COPY_999_1062 (1-64) x US-09-764-875-176 (1-3746)
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                                                                                   Percent Similarity:
                                                                                                       Score:
                                                                                                                                                                       US-09-764-875-176
                                                                                                                                                                                                                                                                                                    Sequence 176, Application US/09764875
publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ02
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                      SEQ ID NO 176
LENGTH: 3746
                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1249
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 193:
                                                                                                                     No.:
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LENGTH: 2873 bases
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9
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REFERENCE/DOCKET NUMBER: 1101-174
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US-10-342-887-1882
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SEQ ID NO 1882
LENGTH: 4053
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APPLICANT: He, Yudong
APPLICANT: Linsley, Pet
APPLICANT: Mao, Mao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: DNA
ORGANISM: Homo sapiens
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514 GGTCCA 519
                                                             454
                                                                                                                              334 GAGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGTTCTGAACAACTTAGCCTTGCA
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                                                                                                                                                 23 ProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu
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                                                                 CAGGCCAGAGGAAAAAAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTTG
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Roberts, Christopher J.
Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
Bernards, Rene
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Linsley, Peter
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                                                                  513
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-868-125
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DB:
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Best Local Similarity:
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US-10-172-118-1882
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                                               APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapp NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 125
LENGTH: 4210
                                                                                                                                                                                                                                                        Sequence 125, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
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LENGTH: 4053
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Publication No. US20030224374A1
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 050/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U61167
DATABASE ENTRY DATE: 2001-06-18
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                                                                                                                                                                                                                                                                                                                                                                                514 GGTCCA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                           454
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Mao, Mao
Roberts, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                      SerPro 64
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Van de Vijver, Marc
Bernards, Rene
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Indels:
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Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                 US-09-720-934-2_COPY_999_1062 (1-64) x US-10-398-885A-15 (1-5828)
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 5828
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Saito, Hirobisa
APPLICANT: Takahasi, Eiki
TITLE OF INVENTION: Method of Testing For Allergic Diseases
FILE REFERENCE: SHIMIZU-07907
CURRENT FAPPLICATION NUMBER: US/10/398,885A
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/JP01/08937
PRIOR PILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: JP 2000-314093
PRIOR FILING DATE: 2000-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(5052)
                                                                                                                                                                                                                                       OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic
                                                                                                                                                                       No.:
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3 GluIleAlaGlnValIIeAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla
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Ogawa, Kaoru
Nagasu, Takeshi
Obayashi, Masaya
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74.19%
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Matches:
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APPLICANT:

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US-09-720-934-2_COPY_999_1062 (1-64) x US-10-259-165-471 (1-852)
                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; LOCATION: (391) ...(391)
; OTHER INFORMATION: n =
US-10-259-165-471
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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SEQ ID NO 471
LENGTH: 852
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CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa FEATURE:
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                                                                      655 TTGĠĊTGAGGCCATĊCAGTCTTATCGTĠCTGAGAGTGAAACTGAGCTĊAACCTĠĠĊÁGCT 714
              44 AlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLys 60
                                                                                                                                                                                   4 IleAlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAlaPro
                                                                                                        GlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeuGln
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Provart, Nicholas
Ricke, Darrell
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Chang, Hur-song
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Cooper, Bret
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o. US20030135888A1
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117.50
59.65%
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NAME/KEY: misc feature
; LOCATION: (391)..(391)
; OTHER INFORMATION: n = any nucleotide
US-10-259-165-143
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Best Local Similarity:
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CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 20
                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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LENGTH: 855
TYPE: DNA
                                                                                                        Sequence 41013, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhu, Tong APPLICANT: Wang, Xu
                                                                    APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
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                                                                                                                                                                                                                                                                                                        769 TGCAGAGGGAAA-----GCTGGCTGGTTCCCTTACGACTACATCGAG
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Zhou, x....
Cao, Yongwei
Wu, Wei
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Katagiri, Fumiyaki
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Cooper, Bret
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Chang, Hur-song
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Query Match: DB:

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Percent Similarity:
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; Sequence 15, Application US/10029386

; Publication No. US20030194704A1
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 41013
LENGTH: 1563
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence Listing SEQ ID NO 15
LENGTH: 564
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                                                                              PERTURE:

PERTURE INFORMATION: MAP TO ALI35783.6

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.55

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.62

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.51

OTHER INFORMATION: SIRPRESSED IN LUNG, SIGNAL = 0.51

OTHER INFORMATION: SIRSPROT HIT 014155, EVALUE 6.00e-27

OTHER INFORMATION: NT HIT: 9114765025, EVALUE 1.00e-110

OTHER INFORMATION: EST_HUMAN HIT F20693.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                       TYPE: DNA
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ORGANISM: Oryza sativa
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
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US-10-425-114-31465
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Best Local Similarity:
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APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5871
LENGTH: 361
GENERAL INFORMATION:
                      Sequence 31465, Application US/10425114 Publication No. US20040034888A1
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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Screen, Steven E
Tabaska, Jack E
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Percent Similarity:
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US-09-720-934-2_COPY_999_1062 (1-64)
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31465
LENGTH: 1420
TYPEP: NAME
                                                                                                                                                                                                                                                                     SEQ ID NO 25238
LENGTH: 1505
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER: OF SEQ ID NOS: 73128
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ORGANISM: Zea mays
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Search completed: July 1, 2004, 20:16:08 Job time : 202.347 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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-Q=/GGM21/USETO_Spool_p/US09720934/runat_30062004_064540_13442/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOGPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human140.cdi -LIST=45
-DCCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000
-USER=US09720934 @CGN 1 1 12421 @runat 30062004 064540 13442 -MCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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-MODEL=frame+_p2n.model -DEV=xlp
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seq length: 2000000000
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Fgapop 6.0 , F
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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283883 4A3B-AAG	281124 4A3A-ABB-	F144063 UI-HF-BP	U106683 602554	U430865 UI-HF-BN	07724 HSC2FG081	F766841 CES003	X276672 BX27	K054527 Mus	944 DKF2	89231 ut64d0	092285 BW0922	AV849639 AV849639	232778 BW2327	86072 AV88607	729475 HS 2154	100 HSC0XA031	252614 HS 2010	.93287 yt69g01.	F763755 CES00544	U451981 6037676	X879964 BX8799	53372 62487	D347867 UI-M	B163763 K-ES	62938	82606 Mus	19029 AG	A987804 AGEN	122946 601	U614534 UI-M-	M950476 UI-M-	U054334 UI-M	BO443095 UI-M-	94919 mi79	63751 mi7901	CGS08946 OSTS9780	809718	D356862 AGEN	F768246 CESO	393010 NISC m	134506 DKFZp547M	B156803 K-EST021	B161912 K-EST02	μ	б	

ALIGNMENTS

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	CA390605	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	EST.	CA390605.1 GI:24721774	CA390605	5', mRNA sequence.	(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs111d07	cs111d07.y1 Human Retinal pigment epithelium/choroid cDNA	CA390605 538 bp mRNA linear EST 06-NOV-2002		

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RESULT 2
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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CB161912
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: graeme@helix.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and splice variants Mol. Vis. 8 (4), 205-220
                                                                         AGCCCT
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301 496 0078
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/note="Organ: Eye; Vector: pCMVSBORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rpokville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen.com/). The library code context of invitrogen.com/). The library code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <http://www.invitrogen.com/>). The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/db_xref="taxon:9606"
/clone="cs111d07"
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                  K-EST0215771 L17N670205n1 Homo sapiens L17N670205n1-4-C07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 Eoeun-dong Yuseong-gu,
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alm, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

Zic Frontier Korean EST Project 2001
Unpublished (2002)
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1 (bases 1 to 545)
Kim, N.S., Hahn, Y., Oh, J.H.,
  CB156803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: yongsung@mail.kribb.re.kr
Plate: 41 row: H column: 01
High quality sequence stop: 545.
Location/Qualifiers
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/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: Not1; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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/db_xref="taxon:9606"
/clone="L17N670205n1-41-H01"
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RESULT 4
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 Homo
              AL134506.1 GI:6602693
EST.
                                                                                          AL134506
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Plate: 4 row: C column: 07
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Fax: +82-42-860-4409
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21C Frontier Korean
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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im,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.I
n.K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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NISC mq28c06.yl NICHD XGC Emb5
IMAGE:5384843 5', mRNA sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Silurana
1 (bases 1 to 628)
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Blum,H., Bauersachs,S., Mewes,W., Weil,B.
EST (Blum,H., Bauersachs,S., Mewes,H.W., Unpublished (1999)
                                                                       Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      Silurana tropicalis (western clawed
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/note="Vector: pAMP1; Site_1: Not1; Site_2:
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/lab host="xll-zblue"
/clone_lib="547 (synonym: hfbrl)"
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/db_xref="taxon:9606"
/clone="DKFZp547M065"
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                                                                                                                    CF768246 629 bp
CDS003921 Bos taurus skin cDNA 1
CCL003921 5', mRNA sequence.
CF768246
CF768246.1 GI:37717465
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DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAMN1980 row: P column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
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National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
 1 (bases 1 to 629) Wang, Y.H., McWilliam, S. Transcription profiling
                                                                                            Bos taurus
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM11980 row: F column: 12
Seq primer: M13RP1 reverse primer (ABI).
                                                Bovidae; Bovinae; Bos.
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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/dev_stage="embryo, stages 10-13"
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/clone_lib="NICHD_XGC_Emb5"
/note="Vector: pcMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV; Cloned_unidirectionally. Primer: OTigo dT. Average insert size 2.0 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
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/db_xref="taxon:8364"
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      31 Rm10A07 Bethesda, MD 20892
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US-09-720-934-2_COPY_999_1062 (1-64) x CF768246 (1-629)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 750)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                   CD356862 750 bp n
AGENCOURT 14253331 NIH MGC_187 Homo
IMAGE:30404497 5', mRNA sequence.
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Contact: Dr Yonghong Wang
Functional Genomics Lab
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Level 5, Queensland Biosciences Precinct,
306 Carmody Road St.Lucia QLD Australia
                                                                                                                                                                                                                                              Homo sapiens (human)
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5 row: A column: 11.
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/note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcoRI;
Site_2: Xho_I; Library made from pooled skin of adult
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/dev_stage="Adult"
/lab_host="XL1-BlueMRF'strain"
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/db_xref="taxon:9913"
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_8118759 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6180303 5', mRNA sequence.

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Unpublished (1999)
                                                                                                                                                                Homo sapiens (human)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/clone lib="NIH_MGC 187"
/note="Organ: Blood_vessels - aorta, basilar and artery;
/note="DNR-LIB; Site 1: Sfil (ggccattatggcc); Site 2:
Sfil (ggccgctcggcc); Si and 3' adaptors were used in
cloning as follows: Si adaptor sequence:
5'-ATCTAGAGGCGACAGGGGGACAGG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
/range 0.5-4.0 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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mol_type="mRNA"
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                                                                                                                                                              CG508946 446 bp OST59780 Mus musculus 1298v/Ev Mus
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Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                genomic survey sequence.
CG508946
CG508946.1 GI:37291689
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High quality sequence stop: 760.
Location/Qualifiers
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                                          Mus musculus
                                                           Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pcwV-SPORT6 (Life Technologies); Si-
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kb for average insert length 1.7 kb. This is a prilibrary, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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clone OST59780,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 537)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sahds, A.T.

Zhu, Q., Person, C. and Sahds, A.T.

while kinase deficiency lowers blood pressure in mice: a gene-trap screen to identity potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                      mj79g10.rl Soares mouse
IMAGE:482370 5' similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zambrowicz BP
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/cell_type="embkyonic stem cell"
/clone_lib="Mus| musculus 129Sv/Ev"
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/mol_type="genomic DNA"
/strain="129SV/EV"
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p3NMF19.5 Mus musculus cDNA clone
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US-09-720-934-2_COPY_999_1062 (1-64) x AA063751 (1-537)
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                                                               AI594919 603 bp mRNA linear EST 15-MAR-20 mj79g10.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:482370 5' similar to TR:042287 O42287 INTERSECTIN.;, mRNA
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                      sequence.
AI594919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham
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The WashU-HHMI Mouse EST Project
AI594919.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                 GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62
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Location/Qualifiers
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314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                   3 GluIleAlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infomimage.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:293114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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1 (bases 1 to 603)
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares mouse p3NMF19.5"
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/db_xref="taxon:10090"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Dr. James Lin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                 GlulleAlaGlnVallleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole brain"
//dev_stage="embryo 15.5 dpc"
//lab_host="DH10B (T1 phage resistant)"
//lab_host="DH10B (T1 phage resistant)"
//clone lib="NIH BMAP EVO"
//clone lib="NIH BMAP EVO"
//note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I Site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Lowa Mouse Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                            (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/db_xref="taxon:10090"
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National Institutes of Health, Mammalian Gene Collection
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Mus musculus (house mouse)
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BU054334.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodeptia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE:6403783 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCCC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                     gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size splected according to mRNA size fraction, ligated with EcDR I adaptor, digested with Not I, and then cloned directiohally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Ipwa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instituties of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole brain"
/dev_stage="embryo_12.5 dpc"
/lab_host="PH10B (T1 phage resistant)"
/clone_lib="NIH_bMAP_FD0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Scares, Genome Research, 6:791-806,
1996. Denatured_mRNa_was_size_fractionated_out_b a l% agarose
                                                                                                                                                                      (NIMH), Hemin Chin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:6403783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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1.17e-27
325.00
98.39%
98.39%
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                   Ph.D., program coordinator."
     694
61
0
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BM950476
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 ProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM950476 732 bp mRNA linear EST 14-MAR-20
UI-M-EH0p-buu-o-05-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
IMAGE:5687260 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
This clone was contributed by the Brain Molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM950476.1 GI:19434066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62
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                      gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I sive Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and ther cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project
                                                                                                                                                                                                                /tissue_type="whole brain"
/dev stage="embryo 18.5 dpc"
/lab_host="DH108 (71 phage resistant)"
/clone_lib="NIH BMAP_BH0P"
/clone_lib="NIH BMAP_BH0P"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note 2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:5687260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia;
  (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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I, and then

System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

FEATURES SOUTCE	C P HEOCXXLXE	RESULT 15 BU614534 LOCUS DEFINITION UI ACCESSION BU6 VERSION BU6 KEYWORDS EST SOURCE MAS	Db 515Qy 63Db 575	QY 23 Db 455 QY 43	US-09-720-934-2 QY 3 G Db 395 G	ORIGIN Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
primer: pYX-5. Location/Quali 1. 782 // Organism="Mus // organism="Mus // organism="Mus // organism="Mus // organism="Mus // organism="Mus // organism="C57BL // db_xref="ftaxo // clone="U1-M-E" // dev_stage="em // lab_host="DHI // lone lib="Nut" // note="Organ: Site_2: Not I; Bonaldo, Lenno 1996. Denature gel. First str	Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Rodentia; S 1 (bases 1 to 782) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Unpublished (1999) Contact: Robert Strausberg, Ph. Bmail: Cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James L CDNA Library preparation: Dr. CDNA Library preparation: Dr. MDA Sequencing by: Dr. M. Bent Clone Distribution: Clone dist from Dr. M. Bento Soares, bento This clone was contributed by (BMAP)	14534 M-EVO-cbg-l-22- M-EVO-cbg-l-22- 14534 14534 GI:232 	CAAGCTCGAGGAAAAA SerPro 64 AGCCCC 580	ProGlyGlnLeuIleLe	-2_COPY_999_1062 GluIleAlaGlnValII GAAATTGCCCAGGTTA	1.25 325. 38.3 98.3 98.3
r: pYX-5. Location/Qualifiers 1782	ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; lammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 782) IH-MGC http://mgc.nci.nih.gov/. Iational Institutes of Health, Mammalian Gene Collection (MGC) Inpublished (1999) Iontact: Robert Strausberg, Ph.D. Imail: cgapbs-r@mail.nih.gov Issue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained Clone Distribution: Clone distribution information can be obtained This clone was contributed by the Brain Molecular Anatomy Project EMAP)	782 bp mRNA linear EST 20-FEB-2003 -0-UI.r1 NIH BMAP_EVO Mus musculus cDNA clone -0-UI 5', mRNA sequence. 280749	CAAGCTCGAGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTA 574 SerPro 64 AGCCC 580	ProGlyGlnLeuIleAeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu 42	2_COPY_999_1062 (1-64) x BM950476 (1-732) GluIleAlaGlnVallleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla 22	Peulli Chii, Fill, program coordinator." e-27 Length: 732 00 Matches: 61 08 Conservative: 0 98 Mismatches: 1 18 Indels: 0 Gaps: 0

oligo-dT primer containing a Not I site. Double stranded CONA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Qy 63 SerPro 64	Db 310 CAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTA 369	250	Qy 23 ProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu 42	Db 190 GAAATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGGTCCCGAACAACTCACCCTGGCT	QY 3 GluIleAlaGlnValIleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla	US-09-720-934-2_COPY_999_1062 (1-64) x BU614534 (1-782)	DB: 13 Gaps: 0	Query Match: 95.31% Indels: 0	Best Local Similarity: 98.39% Mismatches: 1	Percent Similarity: 98.39% Conservative: 0	Score: 325.00 Matches: 61	Pred. No.: 1.35e-27 Length: 782	Alignment Scores:
	TOAIAASHIYIVAILIYSLEULEU 62	GTGGATGGTGGGAAGGAACTG 309	lyGlyTrpTrpGluGlyGluLeu 42	GTCCCGAACAACTCACCCTGGCT 249	lyProGluGlnLeuThrLeuAla 22	782)	0	0	٢	0	61	782	

Search completed: July 1, 2004, 19:48:54 Job time : 1931.25 secs

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370 AGCCCC 375

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Command line parameters:
-MODEL=frame+_p2n.model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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  3470272 seqs,
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323
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                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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gb ov: *
gb ph: *
gb ph: *
gb ph: *
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Institute of Molecular Biology and Genetics of National Academy of
Sciences of Ukraine, 150, Zabolotnogo str., Kiev 252627, Ukraine
Location/Qualifiers
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Slavov,D., Tassone,F., Rynditch,A.V. and Gardiner,K.
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                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 3241)
Sparks_A.B., Hoffman,N.G., McC
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domain-containing proteins
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               Cloning of ligand targets: systematic isolation
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Mammalia, Eutheria, Primates
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Korenberg, J.R. and Chen, X.N.
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                             Kay, B.K.
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                                               Fowlkes, D.M.
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                                                                                                                                                                                                                 Homo sapiens mRNA; cDNA DKFZp686J17173 (
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            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                         Neuherberg,
                                                       Submitted (17-JUN-2003) MIPS,
                                                                     Fobo,G., Han,M. ar Direct Submission
                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 4321)
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                        BX538175.1 GI:31874620
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sequenced by Qiagen
                                                                                 Lauber, J., Bahr, A., Mewes, H.W., Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                           PheAsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTxpLysGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaValCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla
                                                                                                                                                                                                                                                                                                              GAAGTCAATGGACAAGTGGGGCTCTTCCCATCCAATTATGTGAAGCTGACCACAGAC 1578
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mol_type="mRNA"
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(Hilden/Germany) within the cDNA sequencing
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                                                     Ingolstaedter Landstr.1, D-85764
                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                  Weil,B.,
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m clone DKFZp686J17173).
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This clone (DKFZp686J17173) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mlps.gsf.de/proj/cDNA/.
                BD205035
Isolated
leukemia
  BD205035
                                                                                                                                                               GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp
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                                                                                                                                                                                                                                                                                                    GCAGTGTGCCAGGTGATTGGGATGTACGACTACACCGCGCAGAATGACGATGAGCTGGCC 2864
                                                                                                                                                                                                                                                                                                                             AlaValCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla
                                                                                                                                        GAAGTCAATGGACAAGTGGGGCTCTTCCCATCCAATTATGTGAAGCTGACCACAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="intersectin long isoform, differentially spliced"
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/clone_lib="686 (synonym: hlcc3).
DH10B; sites SfiIA + SfiIB"
                     and
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4289
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Leukemia and utilization thereof

Patent: JP 2002511267-A 3 16-APR-2002;
CEDARS SINAI HEALTH SYSTEM ET AL

OS Homo sapiens (human)

PN JP 2002511267-A/3

PD 16-APR-2002

PF 16-APR-1998 US 60/082007

PR 16-APR-1998 US 60/082007

PI JULIE R KORENBERG,XIAO NING CHEN

PC C1201/68,
PC C1201/68,
PC G01033/68/JA61K48/00,C12015/00,C1205/00

CC Isolated SH3 gene relating to myeloproliferative
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Isolated
                               Bukaryota; Metazoa; Chordata; Craniata; Mammalla; Eucheria; Primates; Catarrhin 1 (Dases 1 to 5199)
Korenberg,J.R. and Chen, X.N.
                                                                                                                           BD205033
BD205033.1 GI:33014803
JP 2002511267-A/1.
              Isolated
                                                                                                Homo sapiens
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Mammalla; Eutheria; Primates;
1 (bases 1 to 5195)
Korenberg,J.R. and Chen,X.N.
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JP 2002511267-A/3.
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                                                                                                            sapiens (human)
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G01N33/68//A61K4B/00,C12N15/00,C12N5/00
Teclated SH3 gene relating to myeloproliferative
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16-APR-1998 US 60/082007
JULIE R KORENBERG, XIAO NING CHEN
C12N15/09, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
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gene relating to my utilization thereof
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Location/Qualifiers
1. .5195
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Mismatches:
Indels:
Gaps:
              to myeloproliferative
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Matches:
                                                             Catarrhini;
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                                                                            Vertebrata; Euteleostomi;
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sorders and
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CEDARS SINAI HEALTH SYSTEM ET AL
OS Homo sapiens (human)
PN JP 2002511267-A/1
PD 16-APR-2002
PF 16-APR-1999 JP 2000543610
PR 16-APR-1998 US 60/082007
PI 16-APR-1998 US 60/082007
PI JULIE R KORENBERG, XIAO NING CHEN
PC C12015/09, A01K67/027, C07K14/47, C07K1
PC C1201/68,
PC G10N33/68//A61K48/00, C12N15/00, C12N15
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                                                                                 Guipponi, M., Scott, H.S.,
Antonarakis, S.E.
Direct Submission
                                                                                                                                                                                                                                                    Antonarakis S.E.

Two isoforms of a human intersectin brain-specific alternative splicing Genomics 53 (3), 369-376 (1998)
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 5287)
Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens intersectin AF064243 AF064243.1 GI:3859852
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                           Submitted (05-MAY-1998) Genetics Michel-Servet, Geneva 4 CH-1211,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaValCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla 20
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                                                                                                                                                                         (bases 1 to 5287)
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16-APR-1998 US 60/082007
JULIE R KORENBERG, XIAO NING CHEN
C12N15/09, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
C12Q1/68,
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Location/Qualifiers
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Matches:
Conservative:
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Indels:
                           and Microbiology,
Switzerland
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3692 GAAGTCAATGGACAAGTGGGGCTCTTCCCATCCAATTATGTGAAGCTGACCACAGAC 3748
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                                                                                                                      PheAsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGly 40
                             GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59
                                                                                       TTCAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAGGA
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QSSRLKYRQLENSHDKIMSGHLTGPQARTILMGSSLPAAQLASINVLSDIDODGKLTA
EEFILAMHLI DVAMSGQPLPPVLIPPEY I PPSFRRVFSGSGISVISSTSVDQRLEPEEPV
LEDEQQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEGERLAQLERAEQE
RKERREGEGERAKGLENGENKRENFERGNLELEKRRQALLEQGRKEGERLAQLERAEQE
RNRRQELLNQRNKEQEDIVVLKAKKRLE EEJEALNDEKERREBEKLGDIRCRLTTQRQ
EIESTINKSRELIA LEAITHLQQQLQESQOMLGRLI PEKQILNDQLKQVQONSLHERBELV
TLKRALEAKELARQHLEDQLDEVEKETRSKLQEID I FNNQLKELEBIHNKQQLQKQKS
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KVVYYRALYPFESRSHDEITIQPGDIVMVKGEWVDESQTGEPGGTLKGKTGWFPA
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NYAEKI PENBYPAPAVRVTDSTSAPAPKLALRETPAPLAVTSSEPSTENNWADFSST
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IRKSTSMDSGSSESPASLKRVASPAAKPVVSGEEFIAMYTYESSEQGDLTFQQGDVIL
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RNFFFGGGIDFUTANVEPLAN
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2843. .3019
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EPPKSTALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF
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3326. .3520
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3110. .3286
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3569. .3748
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/tissue_type="brain"
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/mol_type="mRNA"
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chromosome="21"
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Mismatches: Indels:

5381

Length: Matches: Conservative:

Scores:

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AUTHORS
TITLE
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Pucharcos,C., Fuentes,J.J., Casas,C., de la Luna,S., Alcant Arbones,M.L., Soriano,E., Estivill,X. and Pritchard,M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                        /gene="ITSN"
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KVVYYRALYPFESRSHDEITIQEDI VVVKGEBVTALERGERGFTTSNAQEND
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L Patent: JP 2002511267-A 2 16-APR-2002;
CEDDARS SINAI HEALTH SYSTEM ET AL
OS Homo sapiens (human)
PN JP 2002511267-A/2
PD 16-APR-1999 JP 2000543610
PF 16-APR-1999 US 60/082007
PR 16-APR-1998 US 60/082007
PI JULIE R KONENBERG,XIAO NING CHEN
PC C1201/68, A01K67/027,C07K14/47,C07K16/18,C07K19
PC C1201/68, C12015/09,C12N15/09,C12N15/09
CC Isolated SH3 gene relating to myeloproliferativ
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                         21 PheAsnLysGlyGlnIleIleA$nValLeuAsnLysGluAspProAspTrpTrpLysGly 40
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Korenberg, J.R. and Chen
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Key Location/Qualifiers
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16-ARR-1998 US 60/082007
JULIE R KORENBERG,XIAO NING CHEN
CLENIS/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcan
Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M.
Alusplice cloning of human Intersectin (ITSN), a putative
multivalent binding protein expressed in proliferating and
differentiating neurons and overexpressed in Down syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Homo sapiens
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Castelldefels km. 2,7, Barcelona 08907, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 6439)
Pucharcos, C., Fuentes, J.J., Pritchard, M. and Estivill, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens intersectin long AF114487
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s 1 to 6439)
                                                                                                                                                                                                                                                                            KVYYYRALYPPESRSHDBITIQPGDIVMVKGEWVDESQTGEPGWLGGELKGKTGWFPA
NYAEKIPENEVPAPVKPVTDSTSAPAFKLALEFTPAPLAVTSSSETTPNNWADFSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPPVIQPLPAFAHPAATLPKSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVP
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PSNYVKLTTDMDPSQQWCSDLHLLDWLTPTERKRQGYIHELIVTEENYVNDLQLVTEI
                                                                                                                                                                                                                                                                                                                                                                                           TLKRALEAKELARQHLRDQLDEVEKETRSKLQEIDIFNNQLKELREIHNKQQLQKQKS
MEAERLKQKEQERKIIELEKQKEEAQRRAQEKDKQWLEHVQQEDEHQRPRKLHEEEKL
KREESVKKKDGEEKGKQEAQDKLGRLFHQHQEPAKPAVQAPWSTAEKGPLTISAQENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKERERQEQERKRQLELEKQLEKQRELERQREEERRKEIERBAAKRELERQRQLEWE
RNRRQELLNQRNKEQEDIVVLKAKKKTLEFELEALNDKKHQLEGKLQDIRCRLTTQRQ
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269. .5434
                                                                                 FQKPLMESELLTEKEVAMIFVNWKELIMCNIKLLKALRVRKKMSGEKMPVKMIGDILS
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VTKKDGDWWTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEDEQQQLEKKLPVTFEDKKRENFERGNLELEKRRQALLEQQRKEQERLAQLERAEQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (6), 704-712 (1999)
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1 long isoform (ITSN) mRNA,
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CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKWNSNCQFFIRDLEQEVLCITVFERDQ FSPDDFLGRTEIRVADIKKDOGSKGPVTKCLLLHEVPTGBIVVRLDLOLFDEP"

CDS	TITLE I JOURNAL S FEATURES SOUTCE	RCED NE	RESULT 11 AF064244 LOCUS DEFINITION HACCESSION HACCESSION HETWORDS SOURCE ORGANISM HARBERENCE AUTHORS REFERENCE AUTHORS REFERENCE AUTHORS REFERENCE REFERENC	Qy 21 Db 3794 Qy 41 Db 3854	US-09-720-934- Qy 1. Db 3734	ORIGIN Alignment Sco Pred. No.: Score: Percent Simil Best Local S: Query Match: DB:
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ore:	323.00	Matches:	59
cent Similarity: st Local Similarity:		Conservative: Mismatches:	00
ery Match:	100.00% 9	Indels: Gaps:	0
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1 AlaVal 3572 GCAGTG	YsGlnValIleGlyMet GCCAGGTGATTGGGATG	TyrAspTyrThrAla TACGACTACACCGCC	AlaValCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla 20
21 PheAsn! 3632 TTCAAC	ysGlyGlnIleIleAsn hagggccagaTcaTcaac	ValLeuAsnLysGlu GTCCTCAACAAGGA	PheAsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGly 40
41 GluVali 3692 GAAGTC	\snGlyGlnValGlyLeu \arggacaagrggggcTC	PheProSerAsnTy1	GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59
UULT 12 100312 AP000312 UUS AP000312 HOMO Sapiens	120 ens genomic DNA,	bp DNA romosome 21	linear PRI 24-MAY-2003 clone:RP1-201F12, complete

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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Homo sapiens 2,083,744bp genomic DNA of 21q22.1 (REGION:
D21S226-AML CLONE RANGE: Q78C10-£32E9)
published Only in DataBase (1999)
2 (bases 1 to 100000)
2 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                    AP000193 100000 bp DNA
Homo sapiens genomic DNA, chromosome 2:
clone Q78C10-f32E9, segment 20/21, com
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2 (Dases 1 to 12015)
4 (Dases 1 to 12015)
BHATTORI,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                            Homo sapiens
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On May 23, 2003 this segmence version replaced gi:4835681.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
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US-09-720-934-2_COPY_1080_1138 (1-59) x AP000193 (1-100000)
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Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1998)
2 (bases 1 to 114929)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
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This sequence is conducted by Kitasato University JST sequencing Laboratory as a JST sequencing team. Principal Investigator: Yoshiyuki Sakaki Ph.D. Phone: +81-3-5449-5622, Fax: +81-3-5449-5445,
                                                                                                                                    Submitted (11-MAY-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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/db_xref="taxon:9606"
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/map="21q22.1"
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Fax:81-3-5214-8470)
This sequence is conducted by Kitasato University JST sequencing Leam.
Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phome: +81.3-5449-5622, Fax: +81.3-5449-5445,
sakaki@hgc.ims.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by Human Genome Sequencing in ALIS project JST.
                                                                                                                                                          Direct Submission
Submitted (15-APR-1999) Mika Hirakawa, Japan Science and Technology Corporation (UST), Advanced Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151516 bp DN Homo sapiens genomic DNA of 21q22.1, Q78C10-149C3 region, segment 20/20 AP000117
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/mol_type="genomic DNA"
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                                                                                                                           /standard_name="D21S1980"
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site of PCR_primers."
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/note="NIB1972;The location
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/db_xref="GDB:441363"
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/note="Cda0xa03; The location
                                                                                                                                                                                                                           /note="SHGC-2817;The location site of PCR primers."
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| standard_name="D218235"
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Search completed: July 1, 2004, 16:16:09
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-Q=/cgn2 1/USFTO_spool_p/US09720934/runat_30062004_064540_13455/app_query.fasta_1.1386
-Q=/cgn2 1/USFTO_spool_p/US09720934/runat_30062004_064540_13455/app_query.fasta_1.1386
-DB=ISSUEd_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=55ts -STRATT=1 -RND=1 -RATRIX=bloSum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NORM-CONTENEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-484-710-1

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Sequence 34, Appl	equence 5	equence 32	equence 32	equence 50	quence 32	equence 25	equence 1,	equence 68	equence 93	е 1.9	equence 65	equence 18	equence 2,	equence 2,	equence 5,	σ.	equence 2,	equence 45	equence 5,	equence 5,	quence 45	equence 5	e 2	equence 5	equence 1	equence 1	equence 17	equence 1	equence 1	quence 5	equence 5	_

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GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-AP
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
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TELEPHONE:
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KAY, Bria
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VENTION: POLYPEPTIDES HAVING A FUNCTIONAL
VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAY, Brian K. FOWLKES, Dana M.
                                                                                                                         03-APR-1996
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                                                                                                                                                           ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,915A

FILING DATE: 03-APR-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MISCOL'S G 108110
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TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                        REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                                                                                              NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
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EDNESS: single
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VENTION: POLYEPTIDES HAVING A FUNCTIONAL

VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                       (212) 869-8864/9741
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266.00
91.38%
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Conservative:
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Best Local Similarity:
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   Percent Similarity:
                                            Pred. No.:
                                                           Alignment Scores:
                                                                                                   US-08-475-894-3
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Patent No. 5641748
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                                                                                                                                                                                                                             TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,89-
FILING DATE:
CLASSIFICATION: 530
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pair
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                  NAME: Louis Myers
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
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                                                                                                                              TYPE:
STRANDEDNESS: DOI
STRANDEDNESS: DOI
TOTOGY: linear
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Best Local Similari
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                                                                                                                                                                                                                                                             TOPOLOGY: 1
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Louis Myers
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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REGISTRATION NUMBER:
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GENERAL INFORMATION

APPLICANT: Yen-Ming TITLE OF INVENTION:

HSU
THE CAIP-LIKE GENE FAMILY

NUMBER OF SEQUENCES:

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RESULT 7
US-08-475-894-1
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Best Local Similarity:
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Patent No. 5641748
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
                                                                                                                                                                            GENERAL INFORMATION:
                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS
ADDRESSES: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                   APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
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REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
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STATE: Massachusetts
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                                                                                                                                                                                    ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1659 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION: NAME: Louis Myers
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ADDRESSEE: LAHIVE & COCKFIELD
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REGISTRATION NUMBER:
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                                                                                                                APPLICATION NUMBER: FILING DATE:
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DB:
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                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGI
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
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ADDRESSEE: LAHIVE & COCKFIELD
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               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                             TELEPHONE:
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CLASSIFICATION: 435
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STRANDEDNESS: both
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                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)227-7400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM FC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PatentIn Release #1.0, Version PATA:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/474,697 FILING DATE:
                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                   LENGTH: 1659 base pairs
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WENTION: THE CAIP-LIKE GENE FAMILY
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Matches:
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Conservative:
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Indels:
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 Percent Similarity:
Best Local Similarity:
                                                                    Alignment Scores:
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Patent No. 6423824
                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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APPLICATION NUMBER: US,
FILING DATE: 27-JUN-199
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: STREET: Boston
                                                    No.:
                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/484,709
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/475,894
FILING DATE: 07-JAN-1995
APPLICATION NUMBER: US 08/475,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 35,965
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FILING DATE: 07-JUN-1995
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UMBER: US 08/474,697
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ON: THE CAIP-LIKE GENE FAMILY
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Matches:
 Conservative: Mismatches:
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US-09-720-934-2_COPY_1080_1138 (1-59)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yen-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suit
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                     No.:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lir
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REGISTRATION NUMBER:
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                                                          118 GAGGCCATAGTGGAGTTTGACTACCAGGCCCAGCACGATGATGAGCTGACGATCAGCGTG 177
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3 CysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAlaPheAsn 22
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TD NO: 5:
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Matches:
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RESULT 14
US-08-494-709-5
; Sequence 5, Application US/08484709
; Patent No. 5837844
; GENERAL INFORMATION:
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Best Local Similarity:
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REGISTRATION NUMBER: BGP-
REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
TELEPAX: (617)227-5941
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APPLICANT: Yen-Ming
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: LAHIVE & COCKFIELD
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STREET:
Boston
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TOPOLOGY: li
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                                                                                                                                                                                                  GlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGlyGluValAsn 43
                                                                                                      GGCAGGAGAGGTTTGTTCCCTGACAACTTTGTAAGA 273
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                                                                                                                                                                         GAGGCCATAGTGGAGTTTGACTACCAGGCCCAGCACGATGATGAGCTGACGATCAGCGTG 177
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THE CAIP-LIKE GENE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-484-709-5
                                                                                                                                                                                                      Sequence 5, Application US/08474697 Patent No. 6171800
                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                            APPLICANT: Yen-ming Hsu
TITLE OF INVENTION: THE
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                 CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                  STATE:
                                                               STREET: 60 St
CITY: Boston
                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                  02109-1875
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DEDNESS: both
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60 State Street, Suit
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THE CAIP-LIKE GENE FAMILY
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                                                                                  510
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Indels:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,697
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOOPLOGY: linear
MOLECULE TYPE: cDNA
US-08-474-697-5
Search completed: July 1, 2004, 19:54:00 
Job time : 45.3138 secs
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                 178 GGTGAAATCATCACCAACATCABGAAGGAGGATGGAGGCTGGTGGGAGGGACAGATCAAC 237
                                                                 238 GGCAGGAGGTTTGTTCCCTGACAACTTTGTAAGA 273
                                                                                      44 GlyGlnValGlyLeuPheProSbrAsnTyrValLys 55
                                                                                                                                                      24 GlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpTysGlyGluValAsn 43
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Indels:
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Matches:
Conservative:
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Result
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-Q=/cgn2 1/USPTO_spool_p/US09720934/runat_30062004_064541_13481/app_query.fasta_1.1386
-Q=/cgn2 1/USPTO_spool_p/US09720934/runat_30062004_064541_13481/app_query.fasta_1.1386
-DB=Published_Applications_NA -QPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODB=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09720934 @CGN 1_1_1500_@runat_30062004_064541_13481
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                       and is
                                                                                                                                                                   derived by analysis of the total score distribution
Query
Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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323
1 AVCQVIGMYDYTAQNDDELA......GEVNGQVGLFPSNYVKLTTD 59
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Copyright (c) 1993 - 2004 Compugen Ltd
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cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*
cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09A PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09E PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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RESULT 1
US-10-264-049-887
                                                                                        NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 887
LENGTH: 2067
TYPE: num
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 887, Application US/10264049 Publication No. US20040005579A1
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PAl33P1
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(5)
                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            and Antibodies
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Score

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Description

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; NAME/KEY: misc_feature
; LOCATION: (2063)..(2063)
; OTHER INFORMATION: n equals
US-10-264-049-887
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 39, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (2058)..(2058)
OTHER INFORMATION: n equals
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                                                                                                                                                                     COMPUTER REALBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/09/879,957
PILING DATE: 13-Jun-2001
CLASSIFICATION: JUNKNOWN>
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SPARKS, Andrew
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                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                     STATE: New YO COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
              FELEPHONE:
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KAY, Brian K.

FOMIKES, Dana M.

MCCONNELL, Stephen J.

INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

DOMAIN DE INTEREST AND METHODS OF IDENTIFYING AND
(212) 869-8864/9741
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                                                                                                                                         08/630,915
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Indels:
Gaps:
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US-09-879-957-193
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Best Local Similarity:
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                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Verent Application DATA:

Application Number: US/9/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POMAIN OF INTEREST AND METHODS OF IDENTIFYING
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                                                                                                           APPLICATION NUMBER: US 08/630,915 FILING DATE: 03-APR-1996 ATTORNEY/AGENT INFORMATION:
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HOFFMAN, No. US20020034755A1h
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STRANDEDNESS: single
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STATE: New Yor
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STREET: 1155 Avenue of the Americas
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(212) 869-8864/9741
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Best Local Similarity:
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Best Local Similarity:
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Publication No. US20040018969A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3746
TYPE: DNA
ORGANISM: Homo sapiens
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1384 ATCAACGGGTGACTGGTCTCTTTCCTTCAAACTACGTTAAGATGACGACAGAC 1437
                                                                                                                                                          1264 GTATGTCAGGTGATTGCTATGTATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTC
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                             42 ValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59
                                                                                                    22 AsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGlyGlu :::||||||||:::|||||||
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches:
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Indels:
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PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR PAPPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1882
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Best Local Similarity:
Query Match:
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US-10-342-887-1882
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 1882, Application US/10172118 Publication No. US20030224374A1
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
                                                                                                                                                                                                                                                                                APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
                                                                                                               APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
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Roberts, Chris
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Van de Vijver, Marc J.
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4053

TYPE: DNA ORGANISM: Homo LENGTH:

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; TYPE: DNA
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US-09-764-868-125
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 1510
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DATABASE ACCESSION NUMBER: U61167
DATABASE ENTRY DATE: 2001-06-18
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                                                    42 ValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59
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Publication No. US20040053282A1
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APPLICANT:
                CURRENT APPLICATION NUMBER: US/10/085,783A CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: US 60/305,340 PRIOR FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: US 60/275,017 PRIOR FILING DATE: 2001-03-12 PRIOR APPLICATION NUMBER: US 60/271,955 PRIOR APPLICATION NUMBER: US 60/271,955 PRIOR FILING DATE: 2001-02-28
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APPLICANT: Hashid
APPLICANT: Ogawa,
                                                                                                                                                                                                  APPLICANT: Chondrogene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
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TITLE OF INVENTION: Method of Testing For Allergic Diseases
FILE REFERENCE: SHIMIZU-07907
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TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: CDS
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Obayashi, Masaya
Saito, Hirohisa
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Ogawa, Kaoru
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Percent Similarity:
Best Local Similarity:
Query Match:
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; OTHER INFORMATION: n is
US-10-242-535A-37196
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US-09-720-934-2_COPY_1080_1138
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SEQ ID NO 37196
LENGTH: 386
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SEQ ID NO 37196
LENGTH: 386
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFERENCE: 4231/2005 CURRENT APPLICATION NUMBER: US/10/242,535A CURRENT FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
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NAME/KEY: misc feature

LOCATION: (10)...(10)

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CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
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LENGTH: 400
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LOCATION: (9)..(9)
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41 GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeu 56
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US-10-648-593-61
Sequence 61, Application US/10648593;
Publication No. US20040106132A1;
GENERAL INFORMATION:
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Publication No. US20040013663A1
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FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
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PRIOR TILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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LOCATION: (68)..(68)
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US-10-648-593-61
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Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
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TITLE OF INVENTION: IDENTIFICATION OF PREDICTING ACTIVITY OF COMPOUNDS THAT
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,621
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APPLICANT: Hsu, Yen-Ming
THE CAIP-LIKE GENE FAMILY
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                                       APPLICATION NUMBER: US/08/671,354
FILING DATE: 27-JUN-1996
APPLICATION NUMBER: US 08/486,344
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/484,709
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/475,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCTGAACGCCAGACGAGCCGTGTTCCCCCGATAACTTCGTGAAGTTA 192
                                                                                                                                                                                            FILING DATE: 13-May-2002
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
FILING DATE: 07-JAN-1995
APPLICATION NUMBER: US 08/475,710
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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APPLICATION NUMBER: US 08/474,697 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10274/009005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

TELEFAX: 617/542-8906

LENGTH: 3143 base pairs

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                                                APPLICATION DIAGNOSIS and Prognosis of Breast Cancer Patients
FILE REFERENCE: 301-188-99
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
ERIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 187, Application US/10342887 Publication No. US20040058340A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
TYPE: DNA
ORGANISM: Homo sapiens
                      LENGTH: 3348
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
Bernards, Rene
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1105 TGCAAAGTAATA-----TTTCCATATGAGGCACAGAATGATGATGAATTGACAATCAAA 1158
                                                 23 LysGlyGln[|elleAsnValLeuAsnLysGlu-----AspProAspTrpTrpLysGly
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Search completed: July 1, 2004, 20:16:15 Job time: 188.007 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-Q-[cgn2 1/USPT0_spool p/US09720934/runat 30062004 064540 13442/app query.fasta_1.1386
-DB=EST -QFMT=fastap -SUPFIX-sts -MINMATCH=0.1 -LOODECL=0 -LOODEXT=0-TIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALION=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=bto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09720934 @CGN 1 1 12421 @runat 30062004 064340 13442 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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VERSION	ACCESSION			DEFINITION	LOCUS	AI151142/c	RESULT 1	
AI1	AI1	MOd	IMA	qc8	AI1			

KEYWORDS ORGANISM Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordara, Craniata, Vertebrara, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 151142

487 bp mRNA linear EST 28-OCT-1
87804.xl Soares pregnant uterus NbHPU Homo sapiens cDNA clone
9RGE:1721214 3' similar to SW:SHT7 HUMAN Q15811 SH3
WALN-CONTAINING PROTEIN SH3P17. ;, mRNA seguence.
151142 .51142.1 GI:3679611 EST 28-OCT-1998

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RESULT 2
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TITLE
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JOURNAL
                                                                  AUTHORS
                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available toyalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 518 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence step: 444.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih gov_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi|nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                               1 (bases 1 to 545)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                    K-EST0221969 L17N670205n1
L17N670205n1-41-H01 5', mF
Unpublished (2002)
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                    Homo sapiens
                                                                                                                                                  Homo sapiens (human)
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             Frontier Korean EST
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/lab_host="DH10B"
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'sex="female"
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1 Homo sapiens cDNA clone
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K-EST0224708 L17N670205n1 Homo sapiens cDNA clone L17N670205n1-46-D04 5', mRNA sequence.
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Plate: 41 row: H column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +82-42-860-4470
Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kim YS
Genome Research Center
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                 Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
                                                                                                                            Unpublished (2002)
Contact: Kim YS
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: yongsung@mail.kribb.re.kr
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/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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21C Fron
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                                                                                                                                                               Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                             21C Frontier Korean EST Project 2001 Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB156803 583 bp mRNA linear K-EST0215771 L17N670205n1 Homo sapiens cDNA clone L17N670205n1-4-C07 5', mRNA sequence.
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1 (Dases 1 to 583)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
                                                                                                                                                    Fax: +82-42-860-4409
                                                                                                                                                                                                                      Genome Research Center
                                                                                                                                                                                                                                               Contact: Kim YS
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                                                                                                           yongsung@mail.kribb.re.kr
4 row: C column: 07
/organism="Homo sapiens"
/mol_type="mRNA"
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Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996). Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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1 (Dases 1 to 591)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NISC_np01g06.y1 NICHD_HS_Ut1
5', mRNA sequence.
                                                                                                                                                                          Seq primer: M13RP1 reverse primer Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/tissue_type="normal endometrium,
phase, cycle day 13"
/lab host="PH10B (T1-resistant)"
/clone_lib="NICHD_HS_Ut1"
                                                                           /clone="IMAGE:5936818"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="L17N670205n1"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."
                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 TICAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13562 row: n column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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clone IMAGE:6180303 5',
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                                                                                                                                                                                                                                                                                                                   quality sequence start: 116 quality sequence stop: 760. Location/Qualifiers
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/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1; Site 2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                              /tissue type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                            'db_xref="taxon:9606"
                                                                                                                                                                               sex="male"
                                                                                                                                                                                                       clone="IMAGE: 6180303"
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idorsal root ganglion Homo sapiens cDNA
mRNA sequence.
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Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 164)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mau
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                        quality sequence stop: 607.
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               /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_71"
/note="Torgan: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3914940"
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s cDNA clone IMAGE:3914940
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                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 522
High quality sequence stops: 299
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 522 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasce, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Mayra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                    Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8889549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 363)
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yr71d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
IMAGE:210733 5' similar to SP:MYSC_ACACA P10589 MYOSIN IC HEAVY ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGTCAATGGACAAGTGGGGCTCTTCCCCATCCAATTATGTGAAGCTGACCACAGAC
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/dev_stage="20 week-post conception fetus"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
                                                                                                                                                                    /mol_type="mRNA"
/db_xref="GDB:3783574"
                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                  /sex="male"
                                                                                                                                   /clone="IMAGE:210733"
                                                                                                                                                    /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 581)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana, Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                              Plate: 120 row: G column: 3
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                      PCR PRimers
                                                                                                                                                                                                                                         and -minmatch 12 options.
                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa
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 /lab_host="DH10B"
/clone_lib="MARC_;
                                 tissue_type="pooled"
                                                    /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                       organism="Sus scrofa"
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lib="MARC 1PIG"
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Sus.
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/note="Vector: pCMV

SPORT6; Site_1: NotI; Site_2:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal R
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (Dases 1 to 612)

1 (Dases 1 to 612)

Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackembush, J. and Keele, J.W.

Porcine gene discovery by normalized cDNA-library sequencing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                 Plate: 120 row: E column: 4 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called and alt v0.980904.e. Vector identified by cross_matci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG894850.1 GI:14305091
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355615 MARC 1PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST cluster assembly
                                                                                                                                                                                                                                                                                       PCR PRimers
                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12226715
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                                                                                                                                                                                                                                                                                                       -minmatch 12 options
                          /organism="Sus scrofa"
/mol_type="mRNA"
/db_tref="taxon:9823"
/tissue_type="pooled"
/lab_host="PHICB"
/clone_libe="MAHC_lPIG"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
Library_made_fyom_pooled_tissue_from_day_11, 13, 15, 20,
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                                                                                                                                                                                              ocation/Qualifiers
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Best Local Similarity:
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 693)
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//Clome_lib=CCSRQCHN62"
//Clome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9031"
/clone="ChEST381118"
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'strain="White Leghorn, Hisex"
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RESULT 12
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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01-M-FP0-bzu-m-16-0-UI.r1 NIH

IMAGE:6407607 5', mRNA sequence
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national Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
                                                 /dev_stage="embryo 15dpc"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="NH1 BMAP FP0"
/clone_lib="NH1 BMAP FP0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/site_2: Not_I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not_I site. Double strand cDNA was
primer containing a Not_I site. Double strand cDNA was
                   size selected according to mRNA size fraction, 1: with EcoR I adaptor, digested with NotI and then
                                                                                                                                                                                                                                                  tissue_type="whole brain"
                                                                                                                                                                                                                                                                        clone="IMAGE:6407607"
                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
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National Institutes of Health, 1
Unpublished (1999)
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UI-M-FD0-bzh-n-08-0-UI.rl NIH_BWAP_FD0 Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                          This clone was contributed by the Brain Molecular
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                                                                                                                                                                                                                                                                                                                                     primer: pYX-5
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab host="mH108 (T1 phage resistant)"
/clone_lib="NIH_BMAP_FD0"
/note="0rgan: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agar.
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                                                                                                                                                                                  clone="IMAGE:6403783"
                                                                                                                                                                                                                            mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                     organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Mus musculus
                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nhh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodehtia; Sciurognathi; 1 (bases 1 to 782)
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                                                                                                                                                                                                                                                                                             http://image.llnl.gov
                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGAC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
                                                                                                                                                                                                                                              e: LLAM10905 row: e column: quality sequence stop: 716.
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/sex="female, virgin"
/tissue_type="infiltrating
/dev_stage="5 months"
/lab_host="DH1QB"
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                    mol_type="mRNA"
'strain="FVB/N"
                                                                                                                                                                             organism="Mus |musculus"
                                                                                        clone="IMAGE: 4950524"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 TTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGA
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UI-M-EV0-cbg-l-22-0-UI.rl NIH BMAP EV0 MU
UI-M-EV0-cbg-l-22-0-UI 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Dr. James Lin. Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 782)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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BU614534.1
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                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sai.
Site_2: Not1; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. Bento Soares, bento-soares@uiowa.edu
/note="Torgan: brain; Vector: pYX-Asc; Site_1: EcoR I; /note="Torgan: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to BonalIdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded
                                                                                                                                   /db xref="taxon:10090"
/db xref="taxon:10090"
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/dev stagg="embryo 15.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_EV0"
                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

US-09-720-934-2_COPY_1080_1138 (1-59) x BU614534 (1-782) Percent Similarity:
Best Local Similarity:
Query Match:
DB: Pred. No.: Alignment Scores: ORIGIN 1.56e-34 313.00 100.00% 96.61% 96.90% Conservative:
Mismatches:
Indels:
Gaps: Length: Matches: 782 57 0 0

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Š Ъ 487 TTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAAGGA 546 21 PheAsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGly 40

占 Å 547 41 GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59 GAAGTCAGTGGGCAAGTTGGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGAC 603

Search completed: July 1, 2004, 19:49:00 Job time : 1780.84 secs

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Maximum DB seq length: 2000000000
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Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aat39795 Human SH3
Aas84762 DNA encod
Aaz34574 Human SH3
Abk43498 DNA encod
Aai63825 Human pol
Aai39009 Mouse Ese
Aaz39009 Mouse Ese
Aaz39008 Mouse Ese
                                                                                                                 Description
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6	102	707	787	787	182	182	182	182	182	182	182	182	182	182	182	182	182	182	184	184	216	216	216	216	216	216	216	216	216	216	216	Ν	320.5		333	333
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AB516408	AA108779	ABS41962	AAK16598	AAK42353	ABA50277	AAI48432	ABA68217	AAI23124	ABS12930	AAI05376	ABS38434	AAK13119	AAK38849	ABA31807	ABA46803	AAI44852	ABA64683	AAI19657	ABL01994	ABL01995	AAK52332	AAZ39026	AAL47247	AAZ39027	AAZ39010	AAS02055	ADB93268	AAS27090	ABK43586	AAZ39011	AAT39799	AAS84763	AAZ34571	AAZ39024	AAZ34570	AAZ34572
8 Human	08779 Probe	Abs41962 Human liv	6598 Human	k42353	a50277 Huma	3432 Prob	8217 Huma	Aa123124 Probe #13	2930 Huma	5376 Prob	uma	3119 Huma	9949 Hima	1807 Prob	a46803 Huma	144852 Prob	64683 Huma	9657 Prob	01994 Dros	01995 Dros	k52332 Huma	z39026 Mous	147247 Alle	az39027 Mous	239010 Mous	2055 DNA	Adb93268 Himan con	7090 CMA	SER DNA AT	239011 Mouse	t39799 Human cl	s84763 DNA enco	az34571 Human SH	z39024 Mouse Es	z34570 Human s	

a

ALIGNMENTS

RESULT 1 AAT39795

AAT39795 standard; DNA; 1389

BP.

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Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular structural element; malignancy; protein identification; functional domain; protein screening;
               07-APR-1995;
03-APR-1996;
                                       04-APR-1996;
                                                                          W09631625-A1.
                                                                                                                                  Homo sapiens.
                                                                                                                                                cellular signal transduction process; ss.
                                                                                                                                                                                           Human SH3P17 gene.
(CYTO-) CYTOGEN CORP.
                                                         10-OCT-1996.
                                                                                                                                                                                                            19-FEB-1998
                                                                                                                                                                                                            (first entry)
              95US-00417872
96US-00630915
                                      96WO-US004454
                                                                                               /*tag=
                                                                                                                 Location/Qualifiers
                                                                                         /product=
                                                                                                          .1389
                                                                                         "SH3P17"
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AAT39786-T39803 represent novel human and mouse genes encoding Src-
CC homology region 3 (SH3) domain containing proteins that can be used in
CC the method of the invention. SH3 domain containing proteins play a role
CC in signalling and structural elements of cells. The method of the
CC invention is for identifying polypeptides containing functional domains
CC multivalent recognition unit (RW) complex with a number of peptides and
CC complex. The method is based on functional similarities and does not rely
CC complex. The method is based on functional similarities and does not rely
CC on sequence similarities. Prior methods only gave limited success for
CC sequence homology among known SH3 proteins. It has been found that small
CC peptide RUs in multivalent form have reduced specificity for a given
CC particularly suited to screening for polypeptides containing functional
CC domains that are similar to, but not identical in sequence to, the
CC original target functional domain. The new method enables proteins having
CC a common function to be identified. Identification of novel SH3 proteins
CC identified, and their specificities (e.g. pharmacological activities) can
CC identified, and their specificities (e.g. pharmacological activities) can
CC be assessed using the method of the invention
RESULT 2
AAS84762
ID AAS8
XX
AC AAS8
XX
DT 13-F
XX
DE DNA
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 76; Fig 50; 174pp; English
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domain) - comprises detecting sel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1389
                                 13-FEB-2002
 DNA encoding novel human diagnostic
                                                                 AAS84762;
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                                                                                                                                                                                                                                                     LeuGlyGlyGluLeuLysGlyIysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle
                                                                                                                                                                                                                                                                                          actarccagccaggagacaraqrcarggrogargaaagccaaacrcgagagaacccggcrgg
                                                                                                                                                                                                                                                                                                                 ThrIleGlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrp
                                                                                                                                                                                                                                                                                                                                                                          ValLysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle
                                                                                                                                                                                                Pro
                                                                                                standard;
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                                   (first entry)
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100.00%
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                       × AAT39795 (1-1389)
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Conservative:
Mismatches:
Indels:
   protein #20566.
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Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;
                                                forensic;
                    88
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Homo sapiens

WO200175067-A2

30-MAR-2001; 2001WO-US008631. 11-OCT-2001

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

Drmanac RT, Liu C, Tang ΥT

P-PSDB; ABG20575 2001-639362/73.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 20566; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is comply the control of the sequence of the invention. Note: The sequence data for this control of the control of co ftp.wipo.int/pub/published_ pct sequences

Sequence 2874 BP; 940 Ä 679 C; 703 G. 552 Η, 0 ς; 0 Other;

Ş 밁 8 US-09-720-934-2_COPY_740_800 (1-61) x AAS84762 (1-2874) Best Local Similarity: Query Match: 밁 Percent Similarity: Score: No.: 973 913 21 41 \vdash ValLysValValTyrTyrArgAlaLeuTyrProDheGluSerArgSerHisAspGluIle LeuGlyGlyGluLeuLygGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle ThrileGlnProGlyAspileValMetValAspGluSerGlnThrGlyGluProGlyTrp GTAAAAGTGGTGTATTACCGGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAATC ACTATCCAGCCAGGAGACATAGTCATGGTGGATGAAAGCCAAACTGGAGAACCCGGCTGG 1.7e-34 333.00 100.00% 100.00% 100.00% Length: Matches: Conservative: Gaps: Mismatches: Indels: 2874 61 0 0 0

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AAZ34574
                                                                                                 Corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the cargion for low platelets on chromosome 21. Sequencing of 5 different curies of cDNA clone from foetal brain (see AAZ34570-74) suggests that at cargion for low platelets on chromosome 21. Sequencing of 5 different curies of cDNA clone from foetal brain (see AAZ34570-74) suggests that at cargion for low platelets on chromosome 21. Sequencing of 5 different curies of cDNA clone from foetal brain (see AAZ34570-74) suggests that at cargion for low platelets on chromosome 21. Sequencing of 5 different curies at 3 isoforms exist. The invention provides methods for the diagnosis curies of cDNA clone from foetal brain (see AAZ34570-74) suggests that at cargion for 21 invention provides methods for the diagnosis curies and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, carginate themselves; screening for a somatic alteration in the SH3D1A curies and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3D1A curies and colpocephaly and adequacy of a treatment; monitoring curies consider, hashing the progress on megakaryocytic abnormality, myeloproliferative disorder, nematopoietic disorder, platelet disorder or leukaemia; and treatment hashing the progress or megakaryocytic abnormality hashormalive disorder.
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                       disorder, haematopoietic disorder, platelet disorder or leuke treatment of a subject (including a prenatal subject) having megakaryoytic abnormality, myeloproliferative disorder, plat disorder, leukaemia or neural disorder using a nucleic acid expresses SH3DlA or its antisense nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of a non-full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
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Sequence 3231 BP; 1004 A;

721 Ç 712 <u>ن</u> 794 Τ, 0 ٦, 0 Other

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ABK4
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AC ABK4
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DT 05-J
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Best Local Similarity:
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     11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
                                                                                                                                                        19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                      07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                               18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                  17-MAR-2000;
                                                                                                                                                                                                                                                                                                                 16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tood
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2000US-0180628P
2000US-0186350P
2000US-0186350P
2000US-0189874P
2000US-0198129P
2000US-0198129P
2000US-0205515P
2000US-020467P
2000US-0214886P
2000US-0216847P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food preservative;
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26-JUL-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0220964P. 2000US-0224518P. 2000US-0224519P.

14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0225214P. 2000US-0225266P. 2000US-0225267P. 2000US-0225268P. 2000US-0225270P.

2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
2000US-022675P.
2000US-0226881P.
2000US-0226888P.

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08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatcoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
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                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or
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                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                        preservatives.
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2000US-0231414P. 2000US-0232080P.

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2000US-0230437P. 2000US-0230438P. 2000US-0231242P. 2000US-0231243P. 2000US-0231244P. 2000US-0231244P.

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04-FEB-2000
24-FEB-2000
24-FEB-2000
10-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; viruc fungicide; ophthalmological; cytostatic; immunosuppressive; nootrop neuroprotective; antiallergic; hepatotropic; antidiabetic; antibacteri antiparasitic; cardiant; gene therapy; cancer; immune disorder; antiparasitic; cardiant; gene therapy; cancer; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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                2000US-0179065P.
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          The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer,
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                       WO9955728-A2
                                                                                                 antiproliferative;
                                                                                                     regulation; actin cytoskeleton; detection; cancer; EH-domain and SH3-domain regulator of endocytosis;
                                                                                                                                                               Mouse; murine;
                                                                                                                                                                                                 Mouse Esel full length cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of [1] is used to promote endocytosis of selected cells. (Ant) agonists of [1] or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal call division or micration. Vival infection.
                                                                                                                                                                                                                                             28-FEB-2000
                                                                                                                                                                                                                                                                                                                        AAZ39008 standard; cDNA; 5082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutants); (1)-specific antibodies (Ab); sequences antisense to the (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with Esp15 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 40-42; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocytosis, used e.g. for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2272 ACCATCCAGCCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATGG
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                                                                                                                                                    Esel; Ese2; endocytosis; vesicular trafficking;
                                                                                                 antiviral; ss.
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                                                                                                                  infection; anticancer;
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AAZ39025 standard; cDNA; 5144 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (I) or Ab are used to suppress abnormal proliferation of cells that cabe stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection, or abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with Esp15 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5082 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathride endocytosis (as a complex with Force variants)
                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor signalling, tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 38-40;
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05-FEB-1999;
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                                                                                                                                                                ThrIleGlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrp
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AAZ39025;

28-FEB-2000

(first entry)

Mouse Esell coding sequence.

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                                                       US-09-720-934-2_COPY_740_800 (1-61) |x AAZ39025 (1-5144)
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Best Local Similarity:
                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
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P-PSDB; AAY57449.
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05-FEB-1999;
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                                                                                                                            No.:
                                                                                                                                                                        abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission. present sequence represents mouse Esell coding sequence
                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 59-62; 99pp; English.
                                                                                                                                                       Sequence 5144 BP; 1447 A; 1298 C; 1415 G; 984 T; 0 U; 0 Other;
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                    GTAAAAGTGGTATATTACCGA¢CGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATC
  ThrIleGlnProGlyAspIle\(\psi\)alMetValAspGluSerGlnThrGlyGluProGlyTrp 40
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         This is the nucleotide sequence of full-length cDNA (clone 11)

C corresponding to a novel human SH3 gene, termed the SH3D1A gene, that

C contributes to the development of platelets and the pathogenesis of

C leukaemias, both in general and in particular those involving the

C megakaryocytic lineage. The SH3D1A gene maps to the small candidate

C region for low platelets on chromosome 21. Sequencing of 5 different

C sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at

C least 3 isoforms exist. The invention provides methods for the diagnosis

C and treatment of megakaryocytic abnormality, myeloproliferative disorder,

C platelet disorder, acute leukaemia, neural disorders, thromobocytopenia,

C platelet disorder on chromosome 21, low platelets in deletion for 21,

C association of gains in chromosome 21 with leukaemias, neural

C and corresponding cognitive dysfunctions, microcephaly, lissencephaly,

C and colpocephaly. Methods are also provided for: suppressing cells unable

C and colpocephaly. Methods are also provided for: suppressing cells unable

C to regulate themselves; screening for a somatic alteration in the SH3D1A

C gene, monitoring the progress and adequacy of a treatment; monitoring

C tumour risk progress or megakaryoctyic abnormality, myeloproliferative

disorder, haematopoietic disorder, platelet disorder or leukaemia; and

C treatment of a suntisect (including a normalial suntiect) having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SH3D1A cDNA clone 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3D1A gene; human; Down's syndrome; leukaemia;
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   Claim
                  Nucleic acid from the human SH3D1A gene and its products, diagnosis and treatment of myeloproliferative disorders as
                                                                                                                                                                                                                                                                     SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelate disorder; neural disorder; chromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
                                                                                  Korenberg
                                                                                                                                                 16-APR-1999;
                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                        (CEDA-) CEDARS
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                                                                                                                                                                                          W09953062-A2
                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            megakaryocytic abnormality, myeloproliferative disorder, disorder, leukaemia or neural disorder using a nucleic ac expresses SH3D1A or its antisense nucleic acid
                                                              1999-633829/54.
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Fig 5; 99pp; English
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                                                                                                                             98US-0082007P
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                                                                                                                                                                                                                       Location/Qualifiers
208. .3642
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                            useful for
                   leukemia
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RESULT 11
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                                                                                                        antiproliferative; antiviral; ss
                                                                                                                      regulation; actin cytoskeleton; detection; cancer; EH-domain and SH3-domain regulator of endocytosis;
                                                                                                                                                                Mouse; murine;
                                                                                                                                                                                                Mouse Esell cDNA sequence
                                                                                                                                                                                                                                                                          AAZ39024;
                                                                                                                                                                                                                                                                                                           AAZ39024 standard;
                                                                                                                                                                                                                                      28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5199
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                                                                                                                                                    Ese1; Ese2; endocytosis; vesicular trafficking;
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04-NOV-1999

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CC proteins (I) and their splice variants (Ese = EH-domain and 2 cregulator of endocytosis). (I) are involved in regulation of clathrin-cc mediated endocytosis (as a complex with Esplis protein), vesicular crafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, complex with Esplis protein), vesicular cytoskeleton. Generally (I) (or its (ant)agonists, complex mutants); (I)-specific antibodies (Ab); complex expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undestrable endocytosis and resulting complex in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent complex. Generally conditions that can be treated include cancer; cabnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal cell creptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Esell cDNA sequence
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05-FEB-1999;
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                                AAZ34571 standard; cDNA; 5458
AAZ34571
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SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss
                                                                                                                                                                                                                                                                                                           CDS
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                                                                                                                                                                                                                       Korenberg JR,
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                                                                                                                                                                                                                                                                                                                                                                                  cDNA clone
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                                                                                                                                                                                                                                                  98US-0082007P
                                                                                                                                                                                                                                                               99WO-US008371
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267. .3929
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Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.

Claim 2; Fig 8; 99pp; English.

CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that CC contributes to the development of platelets and the pathogenesis of CR leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate CR sizes of CDNA clone from fostal brain (see AAZ34570-74) suggests that at CR sizes of CDNA clone from foetal brain (see AAZ34570-74) suggests that at CR least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CR platelet disorder on chromosome 21 with leukaemias, neural creative disorder, acute leukaemia, neural disorders including brain malformations and corresponding cognitive dysfunctions in chromosome 21 with leukaemias, neural calpocephaly. Methods are also provided for: suppressing cells unable creative themselves; screening for a somatic alteration in the SH3D1A creatment; monitoring the progress and adequacy of a treatment; monitoring treatment of a subject (including a prenatal subject) having treatment, monitoring treatment; monitoring companiaty, myeloproliferative disorder, platelet disorder, platelet calcider, p

Sequence 5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 U; 0 Other;

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Percent Similarity:
Best Local Similarity:
Query Match:
US-09-720-934-2_COPY_740_800 (1-61) x AAZ34571 (1-5458)
                                                              Score:
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                                 1.81e-32
320.50
92.42%
92.42%
96.25%
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Matches:
Conservative:
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RESULT 13
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                                                                                                                                                           sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polynucleotic expression or biological activity. The
         diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 20567; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assebiodiversity.
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23-AUG-2000; 2000US-00649167
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imaging; diagnostic; genetic disorder; ss.
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      Identifying polypeptide(s) having specific functional domain (esp. domain) - comprises detecting selective binding to recognition uni regardless of sequence homology.
                                                                                                                                    07-APR-1995;
03-APR-1996;
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                                                                                                     (CYTO-)
                                                  P-PSDB;
                                                            WPI; 1996-465045/46.
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96US-00630915.
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Claim 76; Fig 58; 174pp; English
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CC AANT39786-T39803 represent novel human and mouse genes encoding SrcCC the method of the invention. SH4 domain containing proteins play a role
CC the method of the invention. SH4 domain containing proteins play a role
CC in signalling and structural elements of cells. The method of the
CC in signalling and structural elements of cells. The method of the
CC invention is for identifying polypeptides containing functional domains
CC of interest (especially SH3 domains). The method comprises contacting a
CC identifying polypeptides having a selective binding affinity for the RU
CC complex. The method is based on functional similarities and does not rely
CC complex. The method is based on functional similarities and does not rely
CC consequence similarities. Prior methods only gave limited success for
CC identifying proteins which contain an SH3 domain due to the minimal
CC sequence homology among known SH3 proteins. It has been found that small
CC geptide RUs in multivalent form have reduced specificity for a given
CC peptide RUs in multivalent form have reduced specificity for a given
CC functional domain compared to monomer RUs. Multivalent RU complexes are
CC particularly suited to screening for polypeptides containing functional
CC contains that are similar to, but not identical in sequence to, the
CC original transduction to be identified. Identification of novel SH3 proteins
CC will be useful for a better understanding of cell growth, malignancy,
CC signal transduction processes, etc. New candidate drugs can be signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) be assessed using the method of the invention

Sequence 2873 BP; 903 A; 506 C; 623 G; 841 T; 0 u; 0 Other;

RESULT 15 AAZ39011 Best Local Similarity: Query Match: DB: В Ś Д S US-09-720-934-2_COPY_740_800 (1-61) Percent Similarity: 뭉 Š Alignment Scores: No.: 288 348 228 43 23 3 ValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIle 22 GGTAGTTTTCAAGGAAATTTTÖGCTGGTTTCCATGCAATTATGTAGAAAAATGCCA 404 GlyGluLeuLysGlyLysThrdlyTrpPheProAlaAsnTyrAlaGluLysIlePro GlnProGlyAsplleValMetValAspGluSerGlnThrGlyGluProGlyTrpLeuGly 42 AATTCTGGAGATATAATTCAGGTTGATGAAAAAACCGTAGGAGAACCTGGTTGGCTTTAT 347 9.09e-19 216.00 74.58% 61.02% 64.86% AAT39799 (1-2873) Conservative:
Mismatches:
Indels:
Gaps: Length: Matches: 2873 36 8 15 61

AAZ39011 standard; cDNA; 3593

28-FEB-2000 (first entry)

Mouse Ese2 coding sequence

regulation; actin cytoskeleton, detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; 4s. Mouse; murine; Ese1; Ese2; enddcytosis; vesicular trafficking;

Mus sp

W09955728-A2

27-APR-1999; 99WO-CA000375

27-APR-1998; 98CA-02230201

> 05-FEB-1999; (HSCR-) HSC RES & DEV LP. 99US-0118739P

Wang W, Sengar

2000-052802/04.

New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection

Claim 25; Page 46-48; 99pp; English.

with Esp15 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab), sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Ese1 is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell infection. Endocytosis may also be regulated, in vivo or in cell contractive Ese mutants, then binding dynamin to the contents. The present sequence encodes mouse Ese2. The present invention specifically describes mammalian Ese1 and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis). complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission cellular Q.

Sequence 3593 BP; 1171 A; 783 Ç 850 G; 789 T; 0 U; 0 Other;

US-09-720-934-2_COPY_740_800 (1-61) x AAZ39011 (1-3593) Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score: 1.2e-18 216.00 75.86% 62.07% Indels: Gaps: Conservative: Mismatches: Matches: Length: 3593 36 8 00

멍 á В 5 2155 TTGGTGAATTACAGAGCACTGTACCCTTTTGAAGCAAGAAACCATGATGAGATGAGTTTT 2214 2215 AGTTCTGGGGATATAATTCAGGTTGATGAAAAAACTGTAGGAGAGCCTGGTTGGCTTTAT 2274 43 GlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle 60 23 3 ValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIleThrIle GlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrpLeuGly 42 22

Search completed: i Job time : 199.286 July 1, 2004, 13:31:47 6 secs

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GGTAGTTTTCAGGGAAAGTTTGGCTGGTTCCCCCTGCAACTATGTAGAAAAAGTG

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Command line parameters:

-MODEL=frame+_D2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09720934/runat_30062004_064539_13422/app_query.fasta_1.1386
-DB=N Geneseq_29Jan04 -QEPMY=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODB=LOCAL -OUTPMT=pto -NORM=set -HABPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09720934 @CGN 1 1_1596 @runat 30062004 064539 13422 -NCPU=6 -ICPU=3
-NO MADAP -LARGEOTERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

RESULT 1 AAT39795 07-APR-1995; 03-APR-1996; 04-APR-1996; 10-OCT-1996. Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy protein identification; functional domain; protein screening; cellular signal transduction process; ss. WO9631625-A1. Homo sapiens. Human SH3P17 gene. AAT39795 standard; DNA; 1389 BP. 19-FEB-1998 AAT39795; (first 95US-00417872. 96US-00630915. 96WO-US004454. Location/Qualifiers /product= /*tag= .1389 entry) "SH3P17"

malignancy;

(CYTO-) CYTOGEN CORP

(UYNC-) UNIV NORTH CAROLINA

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AA AAT39786-T39803 represent novel human and mouse genes encoding Src-
CC homology region 3 (SH3) domain containing proteins that can be used in
CC the method of the invention. SH3 domain containing proteins play a role
CC in signalling and structural elements of cells. The method of the
CC invention is for identifying polypeptides containing functional domains
CC of interest (especially SH3 domains). The method comprises contacting a
CC comultivalent recognition unit (RH) complex with a number of peptides and
CC identifying polypeptides having a selective binding affinity for the RU
CC complex. The method is based on functional similarities and does not rely
CC on sequence similarities. Prior methods only gave limited success for
CC identifying proteins which contain an SH3 domain due to the minimal
CC sequence homology among known SH3 proteins. It has been found that small
CC geptide RUs in multivalent form have reduced specificity for a given
CC particularly suited to screening for polypeptides containing functional
CC gomains that are similar to, but not identical in sequence to, the
CC original target functional domain. The new method enables proteins having
CC a common function to be identified. Identification of novel SH3 proteins
CC will be useful for a better understranding of cell growth, malignancy,
CC signal transduction processes, etc. New candidate drugs can be
CC dentified, and their specificities (e.g. pharmacological activities) can
CC dentified the method of the invention
RESULT 2
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ovarian cancer; breast infertility; pregnancy
   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
                                                                         Human ovarian antigen HVVBX28
                                                                                                                 22-AUG-2002
                                                                                                                                                     ABQ55007;
                                                                                                                                                                                             ABQ55007 standard;
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                                                                                                                                                                                                                                                                                                                                                TTCAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAGGA
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                                                                                                                 (first entry)
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Conservative:
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inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 21q22.1-22.2;
                                                                                                                                                                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                                                                                                                                            PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
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Homo sapiens.

WO200200677-A1

03-JAN-2002

07-JUN-2001; 2001WO-US018569

07-JUN-2000; 2000US-0209467P

(HUMA-) HUMAN GENOME SCI INC

Œ, Rosen CA;

P-PSDB; ABP41930 2002-147878/19.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological ovarian

Claim 1; SEQ ID NO 887; 2922pp; English

cc shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and cyalinitis), immune disorders (e.g., congenital and acquired vaginitis), immune disorders (e.g., congenital and acquired commune disorders (e.g., anaemia), cardiovascular disorders, cc lood-related disorders (e.g., anaemia), cardiovascular disorders, card The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dymenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic chock syndrome) inflammatory conditions (e.g., chlamydia, HIV, toxoplasmosis, and conhoritis and

Sequence 2067 BP; 614 A; 426 <u>.</u> 418 ଦ Η. 0 U;

Percent Similarity: Best Local Similarity: Query Match: DB:	Alignment Scores: Pred. No.: Score:
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RESULT 3
ANA34574
AD ANA33
XX ANA34574
AC ANA33
AC ANA33
AC ANA33
AC Huma
XX SH3D
KW SH3D
KW Megaa
KW Inser
COS
FT CDS
FT
This is the nucleotide sequence of a non-full-length cDNA (clone 9) CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that CC contributes to the development of platelets and the pathogenesis of CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3D1A gene maps to the small candidate CC region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC absociation of gains in chromosome 21, low platelets in deletion for 21, CC abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, CC and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves, screening for a somatic alteration in the SH3D1A cc gene; monitoring the progress and adequacy of a treatment; monitoring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-633829/54.
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                             Nucleic acid from the human SH3DlA gene and its products, diagnosis and treatment of myeloproliferative disorders are {\bf r}
                                                                                                                                                                                                                                                                                                                                      SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; th
                                                                        P-PSDB; AAY32156.
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                                                                                                             Korenberg JR,
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                                                                                                                                                                16-APR-1998;
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CC corresponding to a novel human $H3 gene, termed the $H3D1A gene, that CC contributes to the development of platelets and the pathogenesis of CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The $H3D1A gene maps to the small candidate cregion for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from focetal brain (see AAZ34570-74) suggests that at CC least 3 isoforms exist. The invantion provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and corresponding cognitive dysfunctions, microcephaly, lissencephaly, companies of a treatment; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, leukaemia; and creatment of a subject (including a prenatal subject) having the progress of the subject of a subject (including a prenatal subject) having companies of the subject of an antisense nucleic acid that expresses SH3D1A or its antisense nucleic acid
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01-FEB-2000 AAZ34571;

(first entry)

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RESULT 6
AAZ34571
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AAZ34571 standard;
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                                                                                             GAAGTCAATGGACAAGTGGGGCTCTTCCCCATCCAATTATGTGAAGCTGACCACAGAC 3621
                                                                                                                           GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59
                                                                                                                                                                                             TTCAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAAGGA
                                                                                                                                                                                                                         PheAsnLysGlyGlnTleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGly 40
                                                                                                                                                                                                                                                                                        GCAGTGTGCCAGGTGATTGGGATGTACGACTACACCGCGCAGAATGACGATGAGCTGGCC
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Human SH3D1A cDNA clone

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                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of full-length cDNA (clone 21) corresponding to a novel human SH3 gene, termed the SH3DIA gene, that CC contributes to the development of platelets and the pathogenesis of CC leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DIA gene maps to the small candidate coregion for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at CC least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, clutelet disorder, acute leukaemia, neural disorders, thromobocytopenia, association of gains in chromosome 21 with leukaemias, neural corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable gene; monitoring the progress and adequacy of a treatment; monitoring the progress and adequacy of a treatment; monitoring the progress or megakaryoctyic abnormality, myeloproliferative custored, leukaemia; and megakaryocytic abnormality, myeloproliferative custored, leukaemia; and colpocephaly between the progress or megakaryoctyic abnormality, myeloproliferative custored, platelet disorder, platelet di
                                                                                      US-09-720-934-2_COPY_1080_1138 (1-59)
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                                                                                                                                                                                                                                                                                                               Sequence 5458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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                         AlaValCysGlnValI1eGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla 20
GCAGTGTGCCAGGTGATTGGGATGTACGACTACACCGCGCAGAATGACGATGAGCTGGCC
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The invention relates to isolated polynucleotide (I) and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, compared in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed compared in gene therapy techniques to restore normal compared in the sequence tags for identifying expressed compared in the sequence tags for identifying (II). (II) is compared in the sequence sequence set the sequence and as a food complymential in tissue, as molecular weight markers and as a food complymential in the similar partners are useful in medical imaging constitution of sequence in the sequence have applications in the compared in the sequence in the sequen
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                                                         amino acid sequences. AAS64197-AAS94564 represent novel human diagnocoding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained electronic format directly from WIPO at
                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 20566; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
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23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
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Alignment Scores: Pred. No.:

Sequence 2874

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The present sequence encodes manuse Esel. The present invention consecutive specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and $H3-domain regulator of endocytosis). (I) corriants (Ese = EH-domain and $H3-domain regulator of endocytosis) (as a complex composition of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton. Complex (Espl5) (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I) specific antibodies (Ab); sequences antisense to the (I) correspondents that downregulate expression of Ese genes or complex endocytosis of an Ese binding partner are used to treat diseases antisense to the constitution. Particularly overexpression of Esel is used to block clathring mediated endocytosis in vivo or in cell cultures, while administration of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to promote endocytosis and receptor; and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; murine; Esel; Ese2; endobytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiproliferative; antiviral;
                                                                                                                                                                                                                                                                                New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998;
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99US-0118739P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Espis complex, then binding dynamin to complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3723 BP; 1065 A; 941 C; 1025 G; 692 T; 0 U;
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                                                                                                                                                         Egan
                                                                                                                                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                          Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Esel full length cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ39008;
                                                                                                                                                                                                          27-APR-1998;
05-FEB-1999;
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                                                                                                                       P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA;
                                                                                                                                                         Wang W,
                                                                                                                                                                                    RES
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                                                                                                                                                                                                                      98CA-02230201
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                                                                                     encoding Esel and 2 proteins, involved in regulation of de.g. for treating cancer or preventing viral infection.
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The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis (as a complex are involved in regulation of clathrin-mediated endocytosis).

Claim 6; Page 38-40; 99pp;

English

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RESULT 10
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  WPI; 2000-052802/04
                                                        Egan SE,
                                                                                                          (HSCR-) HSC RES & DEV LP
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05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiproliferative; antiviral; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulation; actin cytoskeleton; detection; cancer; EH-domain and SH3-domain regulator of endocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Esell coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ39025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match:
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                                                  Wang W,
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99US-0118739P
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                                                  Sengar A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator of endocytosis). (I) are involved in regulation of clathrin-
mediated endocytosis (as a complex with Esp15 protein), vesicular
trafficking and actin cytoskeleton. Generally (I) (or its (ann) agonists,
minetics, fragments and inactive mutants); (I)-specific antibodies (Ab);
sequences antisense to the (I) polynucleotide, agents that downregulate
expression of Ese genes or antagonists of an Ese binding partner are use
to treat diseases associated with undesirable endocytosis and resulting
changes in cellular function. Particularly overexpression of Esel is use
to block clathrin-mediated endocytosis in vivo or in cell cultures, whil
administration of (I) is used to promote endocytosis of selected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5144 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins (I) and their splice variants (Ese = EH-domain and
regulator of endocytosis). (I) are involved in regulation of
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GluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp
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                                                                                                                                 GCAGTGTGCCAGGTGATCGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCC
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Matches:
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SH3-domain
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                                                                                                          Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking;
                                                                                  regulation; actin cytoskeleton; detection; cancer; EH-domain and SH3-domain regulator of endocytosis;
                                                                                                                                         Mouse Esell cDNA sequence
                                                                                                                                                                     28-FEB-2000
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                                                                          antiproliferative; antiviral; ss.
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                                                                                                                                                                 (first entry
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GAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGAC 3621

27-APR-1999;

99WO-CA000375

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cc proteins (I) and their splice while the second of capulator of endocytosis). (I) are involved in regulation of clathrin-cc mediated endocytosis (as a complex with Espl5 protein), vesicular cc trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, cc mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); esquences antisense to the (I) polynucleotide; agents that downregulate cc expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting cc changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while capulated capulated endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of (C calls that can be stimulated to proliferate by a growth factor receptor; cand similar compounds (also inactive Ese mutants) can be used to viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; cabnormal cell division or migration; viral infection; or abnormal cell creceptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Esell cDNA sequence
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                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention specifically describes mammalian Esel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY57449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5738
DNA encoding novel human diagnostic protein #20567.
                                   13-FEB-2002
                                                                                                       AAS84763
                                                                                                                                                                              3824
                                                                                                                                                                                                                                                    3764
                                                                                                                                                                                                                                                                                                                       3704 GCAGTGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCC 3763
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                                                                                                                                                                                                                                                                                                                                                 1 AlavalCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 56-59; 99pp; English.
                                                                                                                                                                                                                                                                         PheAsnLysGlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGly
                                                                                                                                                                                                    GluValAsnGlyGlnValGlyHeuPheProSerAsnTyrValLysLeuThrThrAsp 59
                                                                                                                                                                                                                                                    TTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang W, Sengar A;
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100.00%
96.61%
96.90%
                                                                                                         cDNA; 7435
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Indels:
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57
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                       83
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Homo sapiens.

WO200175067-A2

11-OCT-2001

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

Drmanac RI, Liu C, Tang YT;

WPI; 2001-639362/73. DB; ABG20576.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 1; SEQ ID NO 20567; 103pp; English.

cc reaction (PCB) primers, oligomers, and for chromosome and gene mapping, ci n diagnostics as expressed sequence tags for identifying expressed cg enes. (I) is useful in gene therapy techniques to restore normal cg enes. (I) is useful in gene therapy techniques to restore normal cg useful for generating antibodies against it, detecting or quantitating a cg cuspiperide in tissue, as molecular weight markers and as a food cg plypepride in tissue, as molecular weight markers and as a food cg supplement. (II) and its binding partners are useful in medical imaging ci fits expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The camenous for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. AAS6419-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this capatent did not appear in the printed specification, but was obtained in celectronic format directly from MIPO at the invention of the printed specification. The invention relates to isolated polynucleotide (I) and polypeptide (II) ftp.wipo.int/pub/published is useful as hybridisation probes, polymerase chain _pct_sequences

Sequence 7435 BP; 2190 A; 1690 C; 1829 G; 1726 ۲, 0 υ; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-09-720-934-2_COPY_1080_1138 (1-59) x AAS84763 (1-7435) Score: Alignment Scores: No.: 1.24e-33 310.00 98.33% 98.33% 95.98% Length: Matches: Mismatches: Indels: Conservative: 7435 59 0 0 1

8	ДЪ	Q	Db	Ş
40	3818	21	3758	1
40 yGluValAsnGlyGlnValGlyLeuPheProSerAsnTyrValLysLeuThrThrAsp 59	3818 TTCAACAAGGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAGG 3877	21 PheAsnLys-GlyGlnIleIleAsnValLeuAsnLysGluAspProAspTrpTrpLysGl 40	GCAGTGTGCCAGGTGATTGGGATGTACGACTACACCGCGCAGAATGACGATGAGCTGGCC 3817	1 AlaValCysGlnValIleGlyMetTyrAspTyrThrAlaGlnAsnAspAspGluLeuAla 20

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3878

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CC invention is for identifying polypeptides containing functional domains CC of interest (especially SH3 domains). The method comprises contacting a CC multivalent recognition unit (RU) complex with a number of peptides and CC identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely complex. The method is based on functional similarities and does not rely complex. The method is based on functional similarities and does not rely complex. The method is based on functional similarities and does not rely complex. The method sonly gave limited success for complex for proteins which contain an SH3 domain due to the minimal compared to monomer RUs. It has been found that small peptide RUs in multivalent form have reduced specificity for a given comparing that are similar to, but not identical in sequence to, the coriginal target functional domain. The new method enables proteins having common function to be identified. Identification of novel SH3 proteins compared to monomer RUs. Multivalent for over SH3 proteins common function to be identified. Identification of novel SH3 proteins compared to a better understanding of cell growth, malignancy, condentified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention
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AAT39796
                                                                                                                                                                                                                                                                                                                                                 AAT39786-T39803 represent novel human and mouse genes encoding Srchomology region 3 (SH3) domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regardless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying polypeptide(s) having specific functional domain (esp. S domain) - comprises detecting selective binding to recognition unit, regardless of sequence homology.
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03-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy protein identification; functional domain; protein screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 52; 174pp; English
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96US-00630915
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Sequence 747
  B₽;
  244
 A; 133
C; 186
G;
184
T; 0
U; 0 Other;
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Alignment Scores:

AAT39786-T39803 represent novel human and mouse genes encoding Srchomology region 3 (SH3) domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU

76; Fig 58; 174pp; English.

SH3

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03-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                   Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy protein identification; functional domain; protein screening;
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domain) - comprises detecting selective binding to recognition
regardless of sequence homology.
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                                                                                                                                                                                                                                                                                                                                                cellular signal
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96US-00630915
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                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                               transduction
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91.38%
75.86%
82.35%
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672

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RESULT 15
ABK43586
ID ABK43
XX
AC ABK43
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DT 05-J
XX
DT 05-J
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DE DNA
XX
KW Can
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 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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                                                                                                                                                                                                                                                            Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder, Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; sesticular feminisation; endocrine disorder; diabetes; dancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food maintenance; construction; skin aging; food addition; wound healing; cell proliferation; skin aging;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding
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 ; 2000US-0179065P.
; 2000US-018062BP.
; 2000US-0184664P.
; 2000US-0186350P.
; 2000US-0189874P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          novel central nervous system protein #166.
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|G|TATGAACAAAGATGATCCTGATTGGTGGCAAGGAGAG
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2000US-0240960P.
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New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or
                                                                                     WPI; 2001-581633/65.
P-PSDB; AAU87256.
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                                                                                                                                                             Barash SC,
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Alignment Scores: Pred. No.:
                                                     Ce.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, campiogenesis, nervous system disorders e.g. Alzheimer's disease and campiocrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cadenocarcinomas and irritable bowel syndrome, reproductive system conditionates of the calcular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. cespiratory disorders e.g. nonallergic rinhitis, renal disorders e.g. cacute kidney failure and blood related disorders e.g. myocardial conferction. The polypeptides can also be used to aid wound healing and capithalial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                        novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. nepplasms of the breast or liver, cardiovascular disorders
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Ф	8	Db	γQ	Db	Qy	US-09-	B	Query Match:	Best L	Percen	Score:	Pred. No.:
1384	42	1324	22	1264	N	720-934-		Match:	ocal Sim	Percent Similarity:		No.:
ATCAACGG	ValAsnGly	TCCAAGGG	AsnLysGl	GTATGTCA	ValCysGl	2_COPY_1			Best Local Similarity:	rity:		
GTGACTG	GlnValG]	ACAACTCA:	Glnilei	GTGATTG	nVallleG	080_1138	4	82.35%	75.86%	91.38%	266.00	1.09e-27
TCTCTTTC	lyLeuPher	TAATGTT	leAsnValI	TATGTAT	lyMetTyri	(1-59)						27
984 ATCAACGGGGTGACTGGTCTCTTCCTTCAAACTACGTTAAGATGACGACAGAC 1437	roSerAsn	1324 TCCAAGGGACAACTCATTAATGTTATGAACAAGATGATCCTGATTGGTGGCAAGGAGAG	euAsnLys	1264 GTATGTCAGGTGATTGCTATGTATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTC	tq_iAidst	US-09-720-934-2_COPY_1080_1138 (1-59) x ABK43586 (1-3746)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:
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AGATGACG	sLeuThr	TGATTGG	coAspTrp	TGAAGAT	snAspAsp	46)	0	o	5	9	44	3746
ACAGAC 14	ThrAsp 59	: : : rggcaagga	rpLysGly	:::	GluLeuAla							
:37	•	GAG 1	Glu 4	TTC	Phe :							

Search completed: July Job time: 189.112 secs 1, 2004, 13:32:11

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Claim 1; SEQ ID NO 176; 837pp; English

The invention describes an isolated nucleic acid molecule (I)

encoding

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Command line parameters:

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-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_
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ALIGNMENTS

RESULT 1
AAT39795
ID AAT3 07-APR-1995; 03-APR-1996; Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy protein identification; functional domain; protein screening; cellular signal transduction process; ss. (CYTO-) CYTOGEN CORP 04-APR-1996; 10-OCT-1996. WO9631625-A1. Homo sapiens. Human SH3P17 gene. AAT39795 standard; DNA; 1389 BP. 19-FEB-1998 AAT39795; (first 95US-00417872. 96US-00630915. 96WO-US004454. /*tag= /product= "SH3P17" Location/Qualifiers .1389

malignancy;

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AA AAT39786-T39803 represent novel human and mouse genes encoding Src-
CC homology region 3 (SH3) domain containing proteins that can be used in
CC the method of the invention. SH3 domain containing proteins play a role
CC in signalling and structural elements of cells. The method of the
CC invention is for identifying polypeptides containing functional domains
CC of interest (especially SH3 domains). The method comprises contacting a
CC invention is for identifying polypeptides containing functional domains
CC identifying polypeptides having a selective binding affinity for the RU
CC complex. The method is based on functional similarities and does not rely
CC on sequence similarities. Prior methods only gave limited success for
CC identifying proteins which contain an SH3 domain due to the minimal
CC sequence homology among known SH3 proteins. It has been found that small
CC particularly suited to screening for polypeptides containing functional
CC particularly suited to screening for polypeptides containing functional
CC original target functional domain. The new method enables proteins having
CC admains that are similar to, but not identical in sequence to, the
CC original target functional domain. The new method enables proteins having
CC signal transduction processes, etc. New candidate drugs can be
CC identified, and their specificities (e.g. pharmacological activities) can
CC be assessed using the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
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Human SH3D1A cDNA clone 9.
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SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
Homo sapiens
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2. .19. /*tag= Location/Qualifiers
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WO9953062-A2

21-OCT-1999

16-APR-1999;

99WO-US008371

16-APR-1998; 98US-0082007P

(CEDA-) CEDARS SINAI HEALTH SYSTEM.

Korenberg JR,

WPI; 1999-633829/54.

P-PSDB;

Nucleic acid from the human SH3DIA gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.

Claim 2; Fig 14; 99pp; English

CC corresponding to a novel human SH3 gene, termed the SH3DIA gene, that CC contributes to the development of plateletes and the pathogenesis of CR leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from footal brain (see AAZ34570-74) suggests that at CC least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, cCC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CC platelet disorder on chromosome 21 with leukaemias, neural cc abnormalities, dysfunctions and disorders including brain malformations cc and corresponding cognitive dysfunctions, microcephaly, lissencephaly, cc and corresponding cognitive dysfunctions, microcephaly, lissencephaly. CC and corresponding cognitive dysfunctions, microcephaly, lissencephaly. CC and corresponding the progress and adequacy of a treatment monitoring the progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and creatment of a subject (including a prenatal subject) having treatment of a subject (including a prenatal subject) having classification or its antisense nucleic acid that cc expresses SH3DIA or its antisense nucleic acid

Sequence 3231 BP; 1004 A; 721 Ç 712 G; 794 T; 0 ς; 0 Other;

Best Local Similarity: Pred. No.: Query Match: Percent Similarity: 341.00 100.00% 100.00% 100.00% 1.54e-32 Length: Matches: Mismatches: Indels: Gaps: Conservative: 00000

US-09-720-934-2_COPY_999_1062 (1-64) x AAZ34574 (1-3231)

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ARESULT 3
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                                                                                                                  This is the nucleotide sequence of full-length cDNA corresponding to a C covel human SH3 gene, termed the SH3D1A gene, that contributes to the C development of platelets and the pathogenesis of leukaemias, both in CC general and in particular those involving the megakaryocytic lineage. The CC SH3D1A gene maps to the small candidate region for low platelets on CC chromosome 21. Sequencing of 5 different sizes of cDNA clone (see C AAZ34570-74) suggests that at least 3 isoforms exist. The invention CC provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder acute CC leukaemia, neural disorders, thromobocytopenia, platelet disorder on CC chromosome 21, low platelets in deletion for 21, association of gains in CC chromosome 21 with leukaemias, neural abnormalities, dysfunctions and CC disorders including brain malformations and corresponding cognitive GC disorders including brain malformations and colpocephaly. Methods are CC class provided for: suppressing cells unable to regulate themselves; all provided for: suppressing cells unable to regulate themselves; and colpocephaly methods are
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screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring thmour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid from the human SH3DlA gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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       Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human SH3D1A cDNA clone 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ34572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ34572 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                      1999-633829/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                                                                                                                                             CEDARS
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                                                                                                 AAY32156
                                                                                                                                                                        JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                      Chen
                                                                                                                                                                                                                          SINAI HEALTH SYSTEM
                                                                                                                                                                                                                                                                          98US-0082007P
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                                                                                                                                                                                                                                                                                                                         99WO-US008371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5199
64
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Claim

2

Fig 10;

, qqee

English.

Percent Similarity:
Best Local Similarity:

6.69e-31 330.00 100.00% 100.00% 96.77%

Length: Matches: Mismatches: Conservative: Indels:

5195 62

Alignment Scores: Pred. No.:

Sequence 5195 BP; 1592 A; 1148

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1237 G; 1218 T;

0 U;

0 Other;

Query

Match:

US-09-720-934-2_COPY_999_1062 (1-64)

w

Вþ 5

3452 GAAATTGCCCAGGTTATTGCCTCATACACCGCCACCGGCCCGAGCAGCTCACTCTCGCC 3511

GluIleAlaGlnValIleAlaSbrTyrThrAlaThrGlyProGluGlnLeuThrLeuAla

22

x AAZ34572 (1-5195)

This is the nucleotide sequence of full-length cDNA (clone 11)

CC corresponding to a novel human SH3 gene, termed the SH3D1A gene, that

CC contributes to the development of platelets and the pathogenesis of

CC leukaemias, both in general and in particular those involving the

CC megakaryocytic lineage. The SH3H1A gene maps to the small candidate

CC region for low platelets on chromosome 21. Sequencing of 5 different

CC sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at

CC least 3 isoforms exist. The invention provides methods for the diagnosis

CC and treatment of megakaryocytic abnormality, myeloproliferative disorder,

CC platelet disorder, acute leukaemia, neural disorders, thromobocytopenia,

CC platelet disorder, acute leukaemia, neural disorders in deletion for 21,

CC association of gains in chromosome 21 with leukaemias, neural

CC and colpocephaly. Methods are also provided for: suppressing cells unable

CC and colpocephaly. Methods are also provided for: suppressing cells unable

CC regulate themselves; screening for a somatic alteration in the SHJDIA

CC gene; monitoring the progress and adequacy of a treatment; monitoring

CC disorder, haematopoietic disorder, platelet disorder or leukaemia; and

CC megakaryocytic abnormality, myeloproliferative

CC disorder, leukaemia or neural disorder using a nucleic acid that

CC expresses SHJDIA or its antisense nucleic acid

CX expresses SHJDIA or its antisense

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RAESULT 5
AAZ34571
IID AAZ34
XX AAZ3
XX AAZ3
XX O1-F
XX SH3I
KW megg
KW megg
KW plat
KW plat
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XX XX Home
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                                                       SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; heloprosencephaly; diagnosis; th
                                                                                                                                                                                                                                              AAZ34571 standard; cDNA; 5458
                              Homo sapiens
                                                                                                                                                      Human SH3D1A
                                                                                                                                                                                     01-FEB-2000
                                                                                                                                                                                                                 AAZ34571;
                                                                                                                                                                                                                                                                                                                                                                                                                                3512
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                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGTCAGCTGATTTTGATCCGAAAAAAAGAACCCAGGTGGATGGTGGGAAGGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                          GlnAlaArgGlyLysLysArgdlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGlyGlnLeuIleLeuIleAkgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu 42
                                                                                                                                                                                                                                                                                                                                       SerPro 64
                                                                                                                                                                                                                                                                                                         AGCCCT
                                                                                                                                                                                                                                                                                                                                                                   CAAGCACGTGGGAAAAAGCG
                                                                                                                                                        cDNA clone
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                         3637
 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                        AGATAGGCTGGTTCCCAGCTAATTATGTAAAGCTTCTA 3631
                                                                  therapy;
                                                                    88
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Corresponding to a novel human SH3 gene, termed the SH3DIA gene, that Corresponding to a novel human SH3 gene, termed the SH3DIA gene, that Contributes to the development of platelets and the pathogenesis of Cleukaemias, both in general and in particular those involving the Creming for low platelets on chromosome 21. Sequencing of 5 different Sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at cleast 3 isoforms exist. The invention provides methods for the diagnosis can treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21 with leukaemias, neural cashociation of gains in chromosome 21 with leukaemias, neural corresponding cognitive dysfunctions, microcephaly, lissencephaly, and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and corresponding cognitive dysfunctions, microcephaly, lissencephaly, gene; monitoring the progress and adequacy of a treatment; monitoring the progress and adequacy of a treatment; monitoring completed com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of full-length cDNA (clone 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-633829/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korenberg JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY32155
Sequence 5458 BP; 1671 A; 1201 C; 1307 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CEDA-) CEDARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Fig 8; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SINAI HEALTH SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0082007P
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             1279
             Ή,
             0
             U; 0 Other;
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63 SerPro 64	VQ
3615 CAAGCACGTGGGAAAAAGCGCCAGATAGGCTGGTTCCCAGCTAATTATGTAAAAGCTTCTA 367	Дb
43 GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu	γQ
3555 CCTGGTCAGCTGATTTTGATCCGAAAAAAGGAACCCAGGTGGATGGTGGGAAGGAGGCTG 361	Db
23 ProGlyGlnLeuIleLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu 42	Qy
3495 GAAATTGCCCAGGTTATTGCCTCATACACCGCCACCGGGCCCCGAGCAGCTCACTCTCGCC	Db
3 GlulleAlaGlnVallleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla	Qy
US-09-720-934-2_COPY_999_1062 (1-64) x AAZ34571 (1-5458)	US-09-
caps.	DB:
96.77%	Query Match:
ty: 100.00%	Best Lo
Percent Similarity: 100.00% Conservative: 0	Percent
330.00 Matches: 62	Score:
7.12e-31 Length:	Pred. No.:
	Alignment Scores:

42 3554 22

3614

CTTCTA 3674

3675

AGCCCT

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US-09-720-934-2_COPY_999_1062 (1-64)
                                                                                Percent Similarity:
                                                                                                   Score:
                                                                                                                                                                                                                                                  CC variants (Ese = EH-domain and SH3-domain regulator of endocytosis) (I)
C are involved in regulation of clathrin-mediated endocytosis (as a complex
CC with Esp15 protein), vesicular trafficking and actin cytoskeleton.
CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive
CC mutants); (I)-specific antibodies (Ab); sequences antisense to the (I)
CC polynucleotide; agents that downregulate expression of Ese genes or
CC antagonists of an Ese binding partner are used to treat diseases
CC associated with undesirable endocytosis and resulting changes in cellular
CC mediated endocytosis in vivo or in cell cultures, while administration of
CC (I) is used to promote endocytosis of selected cells. (Ant)agonists of
CC (I) or Ab are used to suppress abhormal proliferation of cells that can
CC compounds (also inactive Bse mutants) can be used to prevent viral
CC cultures. by forming an Rse-Fenle complexed to prevent viral
CC cultures. by forming an Rse-Fenle complexed the nivo or in cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
AAZ39009
                                                                    Local
                                                                                                                                                                Sequence 3723
                                                                                                                                                                                                                                                 cultures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specifical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes mouse Esel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY57444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-052802/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1998;
05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HSCR-) HSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiproliferative; antiviral; ss
                                                                                                                                                                                      cell division or migration; viral infection; or abnormal signalling, tissue development or synaptic transmission
                                                                                                                                                                                                                       by forming an Ese-Esp15 complex, then binding dynamin to the Generally conditions that can be treated include cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 40-42; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ly describes mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding sequence
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                                                                                                                                                           BP; 1065 A; 941 C; 1025 G; 692 T;
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                                  1.87e-30
325.00
98.39%
98.39%
95.31%
x AAZ39009 (1-3723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    se Esel. The present invention
Esel and 2 proteins (I) and their splice
                                               Mismatches:
Indels:
                                                                            Conservative:
                                                                                               Matches:
                                                                                                                                                           0 U;
                              001
                                                                            0
                                                                                                                                                           0 Other
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RESULT 7
AAZ39008
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Generally (I) (or its (ant)agonists, mimerics, fragments and inactive mutants); (I) specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Ese is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding dynamin to the
                                                                                                                                                                                                                                     variants (Bse = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex
                                                                                                                                                                                                             with Esp15 protein) Generally (I) (or i
                                                                                                                                                                                                                                                                        The present sequence encodes mouse Esel. The present specifically describes mammalian Esel and 2 proteins
                                                                                                                                                                                                                                                                                                                             Claim 6; Page 38-40; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1998;
05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egan SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1999;
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                                                                                                                                                                                                                                                   invention
(I) and their splice
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                                                                                                                                                                                                                                                                                                                        Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                                                                                                                                                                                                                                                                                                                                                                                     Mouse Esell coding sequence.
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The present invention specifically describes mammalian Ese1 and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-
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05-FEB-1999;
                                                                                                                                                                                                                              27-APR-1999;
                                                Claim 6; Page 59-62;
                                                                         New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection
                                                                                                            P-PSDB;
                                                                                                                                               Egan SE,
                                                                                                                                                                     (HSCR-) HSC RES & DEV LP.
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                                                                                                                        2000-052802/04.
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                                                                                                            AAY57449.
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                                                                                                                                                                                             98CA-02230201.
99US-0118739P.
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325.00
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98.39%
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                                                 99pp; English.
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cc mediated endocytosis (as a complex with Esp15 protein), vesicular crafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, complexics, fragments and inactive mutants); (I)-specific antibodies (Ab); cc sequences antisense to the (I) polynuclectide; agents that downregulate ct treat diseases associated with undesizable endocytosis and resulting cc changes in cellular function. Particularly overexpression of Ese1 is used ct block clathrin-mediated endocytosis in vivo or in cell cultures, while can be stimulated to promote endocytosis of selected cells. Cc (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent cutures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions that can be tracted include cancer; abnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal present sequence represents mouse Ese11 coding sequence

XX Sequence 5144 BP; 1447 A; 1298 C; 1415 G; 984 T; O U; O Other;

Alignment Scores:

2.8e-30

Percent Similarity:

98.39%

Best Local Similarity:

98.39%

Ousery Match:

95.31%

Mismatches:

1

Ousery Match:

95.31%

Mismatches:

1

Ousery Match:

0

US-09-720-934-2_COPY_999_1062 (1-64) x AAZ39025 (1-5144)
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뮍 Ś 밁 Š 밁 8 밁 S 3208 GAAATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGGTCCCGAACACTCACCCTGGCT 3388 3328 3268 43 63 23 w GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62 CCTGGGCAGCTGATTCTGATCCGGAAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACTG AGCCCC 3393 SerPro 64 CAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTA GluIleAlaGlnVallleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla 22 3327 3267 3387

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RESULT 9
AAZ39024
Mus
                                                                                                                Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.
                                                                            WO9955728-A2
                                                                                                                                                                 Mouse Esell cDNA sequence.
                                                                                                                                                                                    28-FEB-2000
                                                                                                                                                                                                       AAZ39024;
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         27-APR-1998;
05-FEB-1999;
                                      27-APR-1999;
                                                          04-NOV-1999
                                                                                               ds
                                                                                                                                                                                                                           standard; cDNA; 5738
                                                                                                                                                                                    (first entry)
           99US-0118739P
                    98CA-02230201.
                                       99WO-CA000375.
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(HSCR-)

HSC RES & DEV

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RESULT 10
ABQ55007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                           Human ovarian antigen HVVBX28 cDNA, SEQ ID NO:887.
                                                                                             22-AUG-2002
                                                                                                                                                                                   ABQ55007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor signalling, tissue development or synaptic transmission. The
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                                                                                                                                                                            standard; cDNA; 2067
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                                                                                                                                                                                                                                                                                                                                                  CAAGCTCGAGGGAAAAAGCGCCAGATAGGGTTGGTTTCCAGCAAATTATGTCAAACTTCTA
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                                                                                        (first entry)
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Percent Similarity: Best Local Similari Query Match:

Similarity:

5.07e-30 319.00 98.39% 95.16% 93.55%

Conservative:

2067 59 2 1 0

No.:

Sequence

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BP;

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U; 4 Other;

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C polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine c disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic c shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and captinitis), immune disorders (e.g., congenital and acquired communities), immune disorders (e.g., anaemia), cardiovascular disorders, conjunctions of communities and confers, autoimmune oophoritis, systemic lupus erythematosus), c blood-related disorders (e.g., anaemia), cardiovascular disorders, ceptiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which communities ovarian antigen expression or activity. The polymucleotides may compound the constitution of individuals and in forensic analysis, and the collection of individuals and in forensic analysis, and the collection of useful in disease diagnosis, drug targeting and phenotyping. The present colly experied the printed specification, but was obtained in electronic format directly from with the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, ar metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to
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RESULT 13
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                       Src-homology region 3 domain; human; mouse; SH3 domain; cell cellular signalling element; cellular structural element; mal protein identification; functional domain; protein screening;
         cellular signal transduction process;
                                                                                                                                                                                                                   AAT39799 standard; DNA; 2873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide RUS in multivalent form have reduced specificity for a given functional domain compared to monomer RUS. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be signal transduction processes, etc. New candidate drugs can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 747 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins which contain an SH3 domain due to the minimal sequence homology among known SH3 proteins. It has been found that small peptide RUs in multivalent form have reduced specificity for a given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 76; Fig 52; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying polypeptide(s) having specific functional domain (esp. S domain) - comprises detecting selective binding to recognition unit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regardless
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                                                                                                                                                                                                                                                                                               514 GGTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transduction processes, etc. New confied, and their specificities (e.g.
                                                                                                                                                                                                                                                                                                                                    SerPro 64
                                                                                                                                                                                                                                                                                                                                                                                        GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                     ProGlyGlnLeuIleArgLysLysAsnProGlyGlyTrpTrpGluGlyGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGTTCTGAACAACTTAGCCTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlulleAlaGlnVallleAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla
                                                                                                                                                                                                                                                                                                                                                             CAGGCCAGAGGAAAAAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTG
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                                                                                                                                             (first entry)
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75.81%
74.19%
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GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62

1119 23

1178

22

GluIleAlaGlnValI1eAlaSerTyrThrAlaThrGlyProGluGlnLeuThrLeuAla

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US-09-720-934-2_COPY_999_1062 (1-64)
                                                    Query Match:
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                                                                                                                       Pred. No.:
                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                    particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be
                                                                                                                                                                                                                                                                                                                     homology region 3 (SH3) domain containing proteins between the method of the invention. SH3 domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins play a role in signalling and structural elements of cells. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). The method comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for sequence homology among known SH3 proteins. It has been found that small peptide RUs in multivalent form have reduced specificity for a given functional domain compared to monomer RUs. Multivalent RU complexes are
                                                                                                                                                                 Sequence 2873 BP; 903 A; 506
                                                                                                                                                                                                be assessed using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT39786-T39803 represent novel human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 76; Fig 58; 174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition unit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regardless of sequence homology.
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03-APR-1996;
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UNIV NORTH CAROLINA
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   x AAT39799 (1-2873)
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                                                                                               Length:
Matches:
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Indels:
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                                                                                   Conservative:
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ins that can be used in
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RESULT 14

AAZ39011;

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Complex. Sequence encouses maybe asset and 2 proteins (I) and their splice consists (Bse = EH-domain and SHI-domain regulator of endocytosis). (I) consists (Bse = EH-domain and SHI-domain regulator of endocytosis) (I) consists (Bse = EH-domain and SHI-domain regulator of endocytosis (As a complex consists (Bse = EH-domain and SHI-domain regulator of endocytosis (As a complex consists); (I) consists (As), sequences antisense to the (I) constants); (I) -specific antibodies (Ab); sequences antisense to the (I) consists of an Ese binding partner are used to treat diseases or consisted with undestrable endocytosis and resulting changes in cellular associated with undestrable endocytosis and resulting changes in cellular consisted endocytosis in vivo or in cell cultures, while administration of consisted endocytosis in vivo or in cell cultures, while administration of constitue to promote endocytosis of selected cells. (Antiagonists of be stimulated to proliferate by a growth factor receptor; and similar compounds (Also inactive Ese mutants) can be used to prevent viral cultures, by forming an Ese-Espli complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer;
   Percent Similarity:
                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Ese2 coding sequence
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05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes mouse Ese2. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Page 46-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HSCR-) HSC RES & DEV LP.
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                receptor signalling, tissue development or synaptic transmission
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                                                                                                                                                                                                                                                                      cell division or migration; viral
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99US-0118739P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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04-FEB-2000;
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                        2000US-0215135P.
2000US-0216847P.
2000US-021680P.
2000US-0217487P.
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2000US-0220963P.
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The invention describes an isolated nucleic acid molecule (I) encoding a CC novel central nervous system protein. (I) and polypeptides (III) encoded CC by (I), are used to treat a medical conditions and in diagnosis of a CC pathological condition. Disorders which are diagnosed or treated include CC pathological condition. Disorders which are diagnosed or treated include CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. caned the collular disorders adenocarcinomas and irritable bowel syndrome, reproductive system CC and pituitary dwarfism, canners and disorders at the cellular level e.g. CC and visual disorders e.g. monallers at the cellular level e.g. respiratory disorders e.g. nonallers rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial cc infarction. The polypeptides can also be used to aid wound healing and
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P-PSDB; AAU87256.
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preventing, additives or

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Search completed: July 1, 2004, 13:32:04 Job time : 205.546 secs	Oy 63 SerPro 64	Oy 43 GlnAlaArgGlyLysLysArgGlnI 	Oy 23 ProGlyGlnLeuIleLeuIleA#gL 	Oy 3 GlulleAlaGlnVallleAlaSerT Oy 3 GlulleAlaGlnVallleAlaSerT Db 1045 GAGATTGCTCAGGTAACTTCAGCAT	(1-64)	CC epithelial cell proliferation, to prevent skin aging due to s CC maintain organs before transplantation, for supporting cell c CC primary tissues, to regenerate tissues and in chemotaxis. The CC polypeptides can also be used as a food additive or preservat cc increase or decrease storage capabilities, fat content, lipid
: 04		GlnAlaArgGlyLysLysArgGlnIleGlyTrpPheProAlaAsnTyrValLysLeuLeu 62 	ProGlyGlnLeuIleLeuIleAfgLySLySASnProGlyGlyTrpTrpGluGlyGluLeu 42	H H	Length: 3746 Matches: 47 Conservative: 7 Mismatches: 8 Indels: 0 Gaps: 0 X ABK43586 (1-3746)	proliferation, to prevent skin aging due to sunburn, to before transplantation, for supporting cell culture of to regenerate tissues and in chemotaxis. The also be used as a food additive or preservative to rease storage capabilities, fat content, lipid, protein,

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ALIGNMENTS

RESULT 1 AAT39795

AAT39795 standard; DNA; 1389 BP

AAT39795;

Homo 07-APR-1995; 03-APR-1996; (CYTO-) CYTOGEN CORP 04-APR-1996; 10-OCT-1996. cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process; ss. WO9631625-A1. Src-homology region Human SH3P17 gene. 19-FEB-1998 sapiens. (first 95US-00417872. 96US-00630915. 96WO-US004454 Location/Qualifiers /product= "SH3P17" /*tag= .1389 3 domain; human; mouse; SH3 domain; cell growth; entry)

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Best Local Similarity:
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SH3DIA gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be assessed using the method
                                                                         Human SH3D1A cDNA clone
                                                                                                            01-FEB-2000
                                                                                                                                                AAZ34574;
                                                                                                                                                                                  AAZ34574 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  676 GTGGAGGGGCTACAAGCTCAAGCCCTATATCCTTGGAGAGCCAAAAAAAGACCACCTTA
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                                                                                                                                                                                                                                                                              GluValGlnGlyGlnLysGly†xpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                             AATTTTAACAAAAATGATGTCATCACCGTCCTGGAACAGCAAGACATGTGGTGGTTTGGA
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Homo sapiens
                                                                                                                                                                                                                                                                                                                             haematopoietic
lissencephaly;
                                                                                                                                                                           Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.
                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                               Korenberg JR,
                                                                                                                                                                                                                                         16-APR-1998;
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                                                                                                                                                                                                                            (CEDA-) CEDARS SINAI HEALTH SYSTEM.
                                                                                                                                                                                                    1999-633829/54.
                                                                                                                                                                                                                Chen X;
                                                                                                                                                                                                                                                                                                                             disorder; cognitive dysfunction; microcephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss
                                                                                                                                                                                                                                         98US-0082007P
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/*tag=
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This is the nucleotide sequence of a non-full-length cDNA (clone 9) corresponding to a novel human SH3 gene, termed the SH3DlA gene, that CC contributes to the development of platelets and the pathogenesis of CP leukaemias, both in general and in particular those involving the CC megakaryocytic lineage. The SH3DlA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different CC sizes of cDNA clone from foetal brain (see ARZ4570-74) suggests that at CP least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CP platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CP platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, CP platelet disorder, acute leukaemia, neural disorders, neural abnormalities, dysfunctions and disorders including brain malformations can dolpocephaly. Methods are also provided for: suppressing cells unable crossing the progress and adequacy of a treatment, monitoring the progress and adequacy of a treatment, monitoring the progress or megakaryoctyic abnormality, myeloproliferative disorder, platelet disorder, leukaemia; and collacorder, leukaemia or neural disorder using a nucleic acid that crossess SH3DlA or its antisense nucleic acid that

Claim 2; Fig 14; 99pp; English.

diagnosis

Sequence 3231 BP; 1004 A; 721 C; 712 G; 794 T; 0 Ų; 0 Other;

Ъ Ś Percent Similarity: Best Local Similari Ś US-09-720-934-2_COPY_908_966 (1-59) x AAZ34574 (1-3231) Query Match: Alignment No.: Similarity: 21 GTGGAGGGGCTACAAGCTCAAGCCCTATATCCTTGGAGAGCCAAAAAAAGACAACCACTTA ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu AATTTTAACAAAAATGATGTCATCACCGTCCTGGAACAGCAAGACATGTGGTGGTTTGGA 1333 AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly 1.8e-36 328.00 100.00% 100.00% 100.00% Conservative: Mismatches: Indels: Length: Matches: 3231 59 0

1273 40

Score: Pred. No.:

Length: Matches:

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RESULT 3
AAZ34572
ID AAZ3
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                                                                                                                                                                    contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of CDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, association of gains in chromosome 21 to platelets in deletion for 21, association of gains in chromosome 2 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and colpocephaly. Methods are also provided for suppressing cells unable to regulate themselves excreening for a scratic alteriation cells unable
                                                       to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platealet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet
                                                                                                                                                                                                                                                                                                                                                                                             corresponding to a novel human SH3 gene, termed the contributes to the development of platelets and the
                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 10; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid from the human SH3D1A gene and its products, us diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CEDA-) CEDARS SINAI HEALTH SYSTEM.
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                                               acid that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukemia
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leukaemia or neural disorder using a SH3D1A or its antisense nucleic acid
  BP;
   1592
 A; 1148 C;
 1237
 G;
 1218
Τ;
0
U; 0 Other
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Sequence 5195

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RESULT 4
AAZ34570
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Best Local Similarity:
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  provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder (
                                      SH3D1A gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention
                                                                               novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage.
                                                                                                                                                                            Nucleic acid from the human SH3D1A gene and its products, diagnosis and treatment of myeloproliferative disorders an
                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                 Korenberg JR,
                                                                                                                                                                                                                                                                                                                        16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megakaryocytic abnormality, myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoletic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy; ss.
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                                                                                                                    is the nucleotide sequence of full-length cDNA corresponding
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thromobocytopenia, platelet
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RESULT 5
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Percent Similarity:
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chromosome
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WPI; 1999-633829/54.
                        Korenberg JR,
                                                                                                                                                                   WO9953062-A2
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                                                     (CEDA-) CEDARS SINAI HEALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAGGGGCTACAAGCTCAAGCCTATATCCTTGGAGAGCCAAAAAAAGACCACCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnPheAsnIysAsnAspVall|eThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGTTCAAGGTCAGAAGGGTTBGTTCCCCCAAGTCTTACGTGAAACTCATTTCAGGG 3105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluValGlnGlyGlnLysGlyTkpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTTAACAAAAATGATGTCATCACCGTCCTGGAACAGCAAGACATGTGGTGGTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21, low
21 with
                                                                                                                                                                                                                                                                                                                               human; Down's syndrome; leukaemia; cancer;
                                                                                                                                                                                                                                                                                                                                                          cDNA clone 21.
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                            Chen X;
                                                                                 98US-0082007P.
                                                                                                            99WO-US008371
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267. .3929
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100.00%
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leukaemias, п
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                                                         SYSTEM
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P-PSDB; AAY32155

Nucleic acid from the human SH3D1A gene and its products, useful for the diagnosis and treatment of myeloproliferative disorders and leukemia.

Fig 8; 99pp; English.

ce megakaryocytic lineage. The SHADIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different ce sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at ce least 3 isoforms exist. The invention provides methods for the diagnosis cand treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, ce platelet disorder on chromosome 21, low platelets in deletion for 21, caspociation of gains in chromosome 21 with leukaemias, neural corresponding cognitive dysfunctions, microcephaly, lissencephaly, and corresponding cognitive dysfunctions, microcephaly, lissencephaly, cand colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA ce disorder, haematopoietic disorder, platelet disorder of eukaemia; and creatment of a subject (including a prenatal subject) having treatment of a subject (including a prenatal subject) having ce megakaryocytic abnormality, myeloproliferative disorder, platelet clisorder, platelet clisorder, leukaemia or neural disorder using a nucleic acid that ce expresses SH3DIA or its antisense nucleic acid This is the nucleotide sequence of full-length cDNA (clone 21) corresponding to a novel human SH3 gene, termed the SH3D1A gene, t contributes to the development of platelets and the pathogenesis cleukaemias, both in general and in particular those involving the of

Sequence 5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 U; 0 Other;

Query Match: Best Local Similarity: Alignment Scores: Percent Similarity: Vo 328.00 100.00% 100.00% 100.00% 2 3.55e-36 Conservative: Mismatches: Indels: Gaps: Length: Matches: 5458 59

US-09-720-934-2_COPY_908_966 (1-59) x AAZ34571 (1-5458)

3123 41 GAAGTTCAAGGTCAGAAGGGTTGGTTCCCCCAAGTCTTACGTGAAACTCATTTCAGGG GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59

멍 Ş 밁 Ş В Ś

AAZ39009 standard; cDNA; ВÞ

AAZ39009;

28-FEB-2000 (first entry)

Mouse Esel coding sequence

RESULT 6
AAZ39009
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX Mous
Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral;

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RESULT 7
AAZ39008
ID AAZ3
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   28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with Esp15 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I) -specific antibodies (Ab); sequences antisense to the (I) polymuclectide; agents that downregulate expression of Ese genes or attagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overrexpression of Ese1 is used to block clathring mediated endocytosis in vivo or in cell cultures, while administration of (I) or Ab are used to suppress abnormal proliferation of cells that can compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may agrowth factor receptor; and similar infection. Endocytosis may also be regulated, in vivo or in cell
                                     AAZ39008;
                                                                 AAZ39008 standard;
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are involved in regulation of clathrin-mediated endocytosis (as a c
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                                                                                                                                                  GluValGlnGlyGlnLysGlyTrpPbeProLysSerTyrValLysLeuileSerGly
                                                                                                                            GAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGG
                                                                                                                                                                                              AATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGA
                                                                                                                                                                                                                     AsnPheAsnLysAsnAspVall1eThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
                                                                                                                                                                                                                                                                                       ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
                                                                                                                                                                                                                                                                GTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAAGACAACCACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 40-42;
(first entry)
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99US-0118739P.
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New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral infection
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                                                                                                                                                                                                                            P-PSDB; AAY57444
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                                                                                                                                                                                                                                                                                                                                                                                      Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Esel full length cDNA sequence
                                                                                                                                                                                    6; Page 38-40;
                                                                                                                                                                                                                                                Wang W,
                                                                                                                                                                                                                                                                              98CA-02230201
99US-0118739P
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                                                                                                                                                                                   99pp; English.
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CC The present sequence encodes mouse Esel. The present invention CC specifically describes mammalian Esel and 2 proteins (I) and their splice CC variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) CC are involved in regulation of clathrin-mediated endocytosis (as a complex CC with Espl5 protein), vesicular trafficking and actin cytoskeleton. CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I) specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular CC mediated endocytosis in vivo or in cell cultures, while administration of CC is used to promote endocytosis of selected cells. (Ant)agonists of SC (I) is used to promote endocytosis of selected cells. (Ant)agonists of SC (I) or Ab are used to suppress abnormal proliferation of cells that can CC compounds (also inactive Ese mutants) can be used to prevent viral compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Esp15 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission Sequence 5082 BP; 1363 A; 1253 C; 1391 G; 1075 T; 0 U; 0 Other,

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AATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTTGGA
                AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly
                                                 GTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAAGACAACCACTTA
                                                                   ValGluGlyLeuGlnAlaGlnAlaLeuTyrProTrpArgAlaLysLysAspAsnHisLeu
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05-FEB-1999;
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Lin cytoskeleton; detection; cancer; infection;
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            The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis (as a complex with Espl5 protein), vesicular creditated endocytosis (as a complex with Espl5 protein), vesicular creditated endocytosis (as a complex with Espl5 protein), vesicular creditated endocytosis (as a complex with Espl5 protein), vesicular creditated endocytosis (as a complex with Espl5 protein), vesicular creditated and inactive mutants), (I)-specific antibodies (Ab); complex endocytosis and sential endocytosis that complex that downregulate endocytosis that can be stimulated with undestrable endocytosis and resulting that can be stimulated to promote endocytosis of Selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of cell wiral infection. Endocytosis may also be regulated by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis that can be regulated, in vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; complex. Generally conditions that can be treated include cancer; the complex of the cancer of the complex of the cancer of the 
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 20567; 103pp; English.
                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to
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23-AUG-2000; 2000US-00649167
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generation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain of indiagnostics as expressed sequence tags for identifying expressed combinant production of the polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed combinated in gene therapy techniques to restore normal combination of the treat disease states involving (II). (II) is considered in tissue, as molecular weight markers and as a food complement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) are useful for treating disorders involving abserrant protein expression or biological activity. The completice and polymucleotide sequences have applications in conditions for exponsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment
Pred. No.:
                                                                                                                                                                                                                                                                                                              RESULT 12
ABA66139
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 395 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                         ABA66139;
                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                               01-FEB-2002
                                                                                30-JAN-2001;
                                                                                                           09-AUG-2001.
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                        Human; foetal
                                                                                                                                                                                                                                                                                                    ABA66139 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                           LeuGluGlnGlnAspMetTrpTkpPheGlyGluValGlnGlyGlnLysGlyTrpPhePro 50
                                                                                                                                                                                                                                                                                                                                                                       LysSerTyrValLysLeuIleSerGly
                                                                                                                                                                                                                                                                                                                                                        AAGTCTTACGTGAAACTCATT
2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                                2001WO-US000669
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                          liver; gene expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 A;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AAI46323
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  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
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04-FEB-2000;
26-MAY-2000;
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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 206
                                                                                                                                                                  Probe; microarray; genetic disorder; s
                                                                                                                                                                                                    Probe #15009 used to measure gene expression in human placenta sample
                                                                                              09-AUG-2001
                                                                                                                    W0200157272-A2
                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                      30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                         GAGGTGCATGGAGGAAGAGGATGGTTTCCCCAAATCTTATGTCAAGATCATTCCTGGG
                                                                                                                                                                                                                                                                                                                                           GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeulleSerGly
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; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
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                                                                      2001WO-US000663.
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                                                                                                                                                                               human; placenta; antenatal diagnosis;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                                                                                                         WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                          hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon nucleic acid probe; liver; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS39875 standard; DNA;
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2000GB-00024263.
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                                                                               hyaline membrane
                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon probe ORF from
                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which associated with coronary heart disease. ABSS5011-ABS51005 represent hum liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printled specification but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS14329
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expression in human adult liver.
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cc derived from human lung, uneasuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a array; identifying exons in a enkaryotic genome, comprising (a) calgorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably the eukaryotic acids from eukaryote lung mRNA, to a single exon probe in the eukaryote; and (b) detecting specific hybridisation of detectably comprising (a) identifying exons to the probe is included in the above mentioned microarray; assigning exons to a single exon probe comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons so a single exon probe with the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon comprosized above and (b) measuring the expression of each of the exons in several the exons should be assigned to a single exon where a common pattern of compression of the exons in the tissues and/or cell types indicates that the exons in the tissues and/or cell types indicates that the exons in the probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human compression of trames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human compression content of the shudy of lung diseases such as asthma, lung called the shudy of lung diseases such as asthma, lung called the exons shudy of lung diseases such as asthma, lung called the exons probe open reading frame of the printed specification, but was obtained in electronic format directly convention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly conventions.
Query Match:
DB:
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of \mbox{single} exon nucleic acid probes, used to measure gene expression in human lung samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 14320; 634pp; English.
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21-SEP-2000;
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2000US-0207456P.
2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000US-0236359P.
; 2000US-00024263.
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                                                                                           GluValGlnGlyGlnLysGlyTrpPheProLysSerTyrValLysLeuIleSerGly 59
                                                                 GAGGTGCATGGAGGAAGGATGGTTTCCCCAAATCTTATGTCAAGATCATTCCTGGG
                                                                                                                                AsnPheAsnLysAsnAspVallleThrValLeuGluGlnGlnAspMetTrpTrpPheGly 40
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spcol_p/IS009720934/Tunat_30062004_064539_13430/app_query.fasta_1.1386
-DB=GenEmbl -QEMT=fastap_SUFFIX=rge_MINWATCH=0.1_-LOOPCL=0_-LOOPEXT=0
-UNITS=bits_START=1_-END=-1_-MATRIX=blosum62_-TRANS=human40.dd_-LIST=45
-DCCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15_-MODE=LOCAL
-UCTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXLEN=2000000000
-USER=US09720934_@CGN_1_1_7509_@runat_30062004_064539_13430_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG
-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_
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/tissue_type="kidney"
/dev_stage="12 week-old embryo"
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Ex Korenberg, J.R. and Chen, X.N.

Isolated SH3 gene relating to myeloproliferative disorders and leukemia and utilization thereof

Patent: JP 2002511267-A 5 16-APR-2002;

CEDARS SINAI HEALTH SYSTEM ET AL

OS Homo sapiens (human)

PN JP 2002511267-A/5

PD 16-APR-2002

PD 16-APR-2002

PD 16-APR-1999 JP 2000543610

PR 16-APR-1998 US 60/082007

PI JULIE R KORENBERG, XIAO NING CHEN

CI2N15/09, A01K67/027, C07K14/47, C07K16/18, C07K19/00, C12N5/10,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Isolated SH3 gene relating to myeloproliferative disorders and leukemia and utilization thereof.
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Human SH3 domain-containing protein SH3P17 mRNA, complete U61166 U61166.1 GI:1438932
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Isolated SH3 gene relating to myeloproliferative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                    41 LeuGlyGlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle
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Mus musculus Esel protein
AF132478
AF132478.1 GI:4378884
                                                       AF132478
                                                                                                                                                    Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3241)
Pirozzi,G., McConnell,S.J., Uveges,A. and Fowlkes,D.M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sparks, A.B., Hoffman, N.G., McConnell, S.J., Fowlkes, D.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3241)
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                                                                                                                       CCA
                                                                                                                                                                              CTTGGAGGAGATTAAAAGGAAAGACAGGGTGGTTCCCTGCAAACTATGCAGAGAAAATC
                                                                                                                                                                                                                                              ACTATCCAGCCAGGAGACATAGTCATGGTGGATGAAAGCCAAACTGGAGAACCCGGCTGG
                                                                                                                                                                                                                                                                  ThrIleGlnProGlyAspIleValMetValAspGluSerGlnThrGlyGluProGlyTrp
                                                                                                                                                                                                                                                                                                             GTAAAAGTGGTGTATTACCGGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAAATC
                                                                                                                                                                                                                                                                                                                                    ValLysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle
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Biotechnol. 14 (6), 741-744 (1996)
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LTLAPGQLILLEKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTEPPK
STALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLFPSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHQRPRKLHEEEKLKREESVKXKDGEBKGKQBAQDKLGRLFHQHQEPAKPAVQAPWST
AEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEBGBLGGEL
KGKTGMFPANYAEKIPENEVPAPVKPVTDSTSAPAPKLALRETPAPLAVTSSEPSTTP
NUWADFSSTWPTSTNEKPETDWDAWAAQPSLTVPBAGGQLRQRSAFTPATATGSSPSP
VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDWWWFGEVQGXGWFPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="SH3 domain-containing protein SH3p17"
/protein_id="AAC50592.1"
/db_xref="GI:1438933"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db xref="taxon:9606"
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                                                3723 bp
                                mRNA,
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Query Match:
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Research/Developmental Biology, The Hospital for Si
University Avenue, Toronto, ON MSG-1X8, Canada
Location/Qualifiers
                           LeuGlyGlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle
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Direct Submission
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The EH and SH3 domain Ese proteins
  ĊTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATT
                                                                                     ACCATCCAGCCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGGATGG
                                                                                                                                                                                                   ValLysValValTyrTyrArgAlaLeuTyrProPheGluSerArgSerHisAspGluIle
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1 (bases 1 to 3723)
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RRQELIANGRIKEGEGTYULKARRKTILEFELEALINKKHOLEGKIODIRCRIANGAN
IKRALELINGRIKEGEGTYULKARRKTILEFELEALINKKHOLEGKIODIRCRIANGAN
IKRALELINGRIKEGEGTYULKARRKTILEFELEALINKKHOLEGKIODIRCRIANGAN
IKRALEAKELARQOLREOLDEVERETRS KLOBILOVENIOLKELKEIHSKOOLOKORSI
EAARILKOKEORKS LELIEKOKEDAORRYOCHENOWILEHVOOBEODER PROHEEDBILKR
EDSVEKKEAEBRAKPEMODKOSRIFHPHOEPAKIATOAPMSTTEKGPLITISAQESVKY
VYYRALYPEBSRSHDEITIQFGDIVMVDESQTOSEPGMIGGELKGATGMEPANYABKIP
ENEVETPAKRYVDLITSAPAPKIALHESTPALPVTSSEBSTTENNMADESSTWESSINE
KPETDNWDTWAAQPSLITVESAGOLRORSAFTPATATGSSESTENNMADESSTWESSINE
KPETDNWDTWAAQPSLITVESAGOLRORSAFTPATATGSSESTENNMADESSTWESSINE
KPETDNWDTWAAQPSLITVESAGOLRORSAFTPATATGSSESGODLTFOOGDVIVVTKKOGD
WWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKREIAQVIASYAATGPEDLITI
APGQLILIRKKNDGGWEGELQARGKKROIGWFPANYYKLSPOTSKITPTELPRITAV
APGQLILIRKKNDGGWEGELQARGKKROIGWFPANYYKLSPOTSKITPTELPRITAV
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QSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTA
EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSTERKRVRSGSGMSVISSSSVDQRLPEEPS
SEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLERAEQER
KERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIERRBAAKRELERQRQLEWER
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RNF5FQsgleQpvlaQiwaladmnndgrmdgvefsiamkliklklggyglpstlppvm
RQQFvaissapafgiggiasmppltavapvpmgsipvvgmspplvssvppaavpplan
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/protein_id="AAD19746.1"
/db_xref="GI:4378885"
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Rodentia;
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Indels:
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Matches:
Conservative:
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Sciurognathi; Muridae; Murinae; Mus
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Sengar, A.S., Wang, W.,
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TAWVQKIKAASELY<sup>†</sup>ETEKKKREKAYLVRSQRATGIGRLMVNVVEGIELKPCRSHGKS
NPYCEVTMGSQCHI<sup>†</sup>KTIQDTLNPKMNSNCQFFIRDLEQEVLCITVFERDQFSPDDFL
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Alignment Scores: Pred. No.:

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Length:

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Isolated SH3 gene relating thereof
leukemia and utilization thereof
Patent: JP 2002511267-A 3 16-APR-2002;
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Korenberg, J.R. and Chen, X.N.
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Mammalia; Eutheria; Primates;
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JULIE R KORENBERG,XIAO NING CHEN
C12N15/09,A01K67/027,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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/db_xref="taxon:9606"
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project
This clone (DKFZp686J17173) is available at the RZDD in Berlin. Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BX538175
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/dev_stage="adult"
/gene="DKFZp686J17173"
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/mol_type="mRNA"
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Mammalia; Butheria; Rodentia; Sciur
1 (bases 1 to 475)
Skripkina,I., Tsyba,L., Slavov,D.,
Novel splicing forms of human and n
                                                                                                                                                                                                                                                                              Submitted (27-UIN-2002) Department of Molecular Oncogenetics, Institute of Molecular Hiology and Genetics of National Academy of Sciences of Ukraine, 150, Zabolotnogo Str., Kiev 03143, Ukraine Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Skripkina, I., Tsyba, L. and Rynditch, A. Direct Submission
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AY127576.1 GI:25989570
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                                                                                                                                              /gene="Itsn"
                                                                                                                                                               /tissue_type="brain"
<1. .>475
                                                                                      /note="alternatively spliced"
/codon_start=1
                                                                                                                   gene="Itsn"
                                                                                                                                                                                            /db_xref="taxon:10090"
/chromosome="16"
                                                                                                                                                                                                                                                    organism="Mus
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Antonarakis,S.E.
Two isoforms of a human intersectin (ITSN) protein in
brain-specific alternative splicing in a stop codon
Genomics 53 (3), 369-376 (1998)
                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (05-MAY-1998) Genetics and Microbiology,
Michel-Servet, Geneva 4 CH-1211, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                            /map="21222.1-q22.2"
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/dev_stage="fetus"
107. .3769
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RQQPVALSSAPPFGMGGIASMPPLTAVAPVPMGSIPVVGMSPTLVSSVPTVAEWAVP
GAPPVIQPLPAFAHPAATLPKSSSFSRSGPGSQLNTKLQKAQSEDVASVPVAEWAVP
QSSRLKYRQLFNSHDKIMNSGHLTGPQAATTILMQSSLPQAQLASIWNLSDIDQDGKLTA
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                codon_start=1
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M.

Alu-splice cloning of human Intersectin (ITSN), a putative
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TLKRALEAKELARQHLRDGLDEVEKTISKLQEID I FINGOLKGULQUNSLHRDSLY

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GLOAQALY PMRAKKDNHLNENUKDVITVLEQODMWMFGEVQGOKGMFPKSYVKLISGP

IRKSTSMDSGSSES PASLKRVASPAKFVVSGEEFIAWTYESSEQGDLTFQCGDVIL

VTKKDGDWMTGTVDGDKAGVFPSNYVRLKDSGGSTAGKTGSLGKKPEIAQVIASYTAT

GPEQLTLAPGQLLLIRKNPGGWMEGELQARGKKRQIGWFPANYVKLLNPGTSKITPT

EPPKSTALAAVCQVIGWYDYTAQNDDELAFNKGQIINVLNKEDPDWMKGEVNGQVGLF

DONNUT TMTNANDSCOM
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3110. .3286
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2324. .2524
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767. .1936
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EIESTNKSRELRIAEITHLQQOLGESQOMLGRLIFEKQILINDQLKQVQQNSLHROSLV
TLKRALEAKELARGHLAGOLDEVEKETISKLQETIDIFNNQLKELERINKOQLQKOKG
MEAERLKQKEQERKIIELEKQKEEAQRRAGEROKQWLGHVQQEDEHQRPRKLHEEEKL
KREGSVKKNOGEEKGKQEAQDKLGRLFHQHQEPAKHAHVQQEDEHQRPRKLHEEEKL
KREGSVKKNOGEEKGKQEAQDKLGRLFHQHQEPAKPAVQAPWSTAEKGPLITISAQENV
KVVYKRALYPFESRSHDEITIQPGDIVMVKGEWDDESQTGEPGHLGGELKGKTGWPPA
NYAEKLIPENEVPAPVKEVTOSTSAPAKKLALAETPAPLAVTSSEPSTTPNNWADESST
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GPEGLTLAPGQLILIRKKNPGGWWEGEELQARGKKRQIGWFPANYVKLLSPGTSKITPT
EPPKSTALAAVCQVIGWYDAYAQNDDELAFNKGQIINVLIKEDPDWWKGEVNGQVGLF
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/mol_type="mRNA"
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Korenberg, J.R. and Chen,
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                                                                                                                              TyrAlaGluLysIlePro 61
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                                                                                                                                                                                                                      GlyGluProGlyTrpLeuGlydlyGluLeuLyBGlyLyBThrGlyTrpPheProAlaAsn 55
                                                                                              TATGCAGAGAAAATCCCA 2681
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G01N33/68/A61K48/0b,C12N15/00,C12N5/00
Isolated SH3 gene relating to myeloproliferative disorders and
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16-APR-1998 US 60/082007
JULIE R KORENBERG,XIAO NING CHEN
C12N15/09,A01K67/02P,C07K14/47,C07K16/18,C07K19/00,C12N5/10,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alcant Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Pucharcos, C., Fuente
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/protein_id="AAD29952.1"
/db_xref="01:4808823"
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/mol_type="mRNA"
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Antonarakis, S.E.
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ipponi,M., Scott,H.S.,
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RKERERGGEGERKGLELEKGRALEGREEERRKEIERRBAKRELERQRQLEWE
RNRRQELLNQRNKEQEDIVVLKAKKKTLEFELBALNDKHQLEGKLQDIRCRLTTQRQ
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TLKRALEAKELARQHLRDQLDEVEKETRSKLGEIDIFENNQLKEELREHNKQQLQKKS
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                                                                                                                                                                                                                                                                                                         /map="21q22.1-q22.2"
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                                                                                                                                                                                                                                                                                                                                                                        chromosome="21"
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US-09-720-934-2_COPY_740_800 (1-61) x AF064244 (1-7247)
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Kenopus laevis intersectin mRNA,
AF032118
AF032118.1 GI:2642624
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NEGTHENDRAUVVYTLR
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/note="encodes
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-OCT-1997) pharmacology, University of Wisconsin, 1300
University Ave, Madison, WI 53706-1532, USA
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 4103)
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Hoffman, N.G., Hardison, N.L., Yamabhai, M. and Kay, B.K.
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                                                                                                                                                                                                                                                                                                           /function="involved in endocytosis"
/note="EH domaih and SH3 domain containing protein;
similar to intersectin binding proteins Ibpl, encoded by
GenBank Accession Number AF057285, and Ibp2, encoded by
GenBank Accession Number AF057286, and mouse
Rab/Rlp,encoded by GenBank Accession Number AF057287"
                                                                                                                                                                                                                                                                TGVFPSNYVRFKDS#AAGSGGKTGSLGKKPEIAQVIASYAATAPEQLTLAPGQLILIR
KKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTNKSTPTEPPKPTSLPPTCQVIG
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                                                                                                               /note="encodes | 2881. .3057
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3607. .3786
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1_type="oocyte"
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                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                  2386 GTGAAGGTTGTATTACCGAGCACTCTACCCTTTTGATGCCCGAAGTCATGATGAAATC
                                                  2506
                                                                                                 2446 ACTATTGAGCCTGGRGACATTATCATGGTGGATGAAAGCCAAACYGGAGAGCCTGGGTGG
2566 CCC 2568
                                                                                                                                                                                                                                                     Similarity:
                         61
                                                                           41
                                                                                                                  21 ThrileGlnProGlyAspileValMetValAspGluSerGlnThrGlyGluProGlyTrp 40
                                                                                                                                                                        1 ValLysValValTyrTyrArgAlaLeuTyrPropheGluSerArgSerHisAspGluIle
                          Pro
                                                CTGGGAGGTGAACTGAAAGGAAAAACGGGCTGGTTTCCTGCCAACTATGCAGAGCGAATG 2565
                                                               LeuGlyGlyGluLeuLysGlyLysThrGlyTrpPheProAlaAsnTyrAlaGluLysIle 60
                          61
                                                                                                                                                                                                                            5.79e-31
317.00
100.00%
90.16%
95.20%
5
                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                4103
6
0
0
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2445

2505

Search completed: July Job time: 1402.43 secs 1, 2004, 16:14:22